

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2002, 05:15:37 ; Search time 1541.15 Seconds

(without alignments)
22372.323 Million cell updates/sec

Title: US-09-636-826-1
Perfect score: 2090
Sequence: 1 GATATCACACATTCGTCAT.....TCGGCTTTCGGCTGCTGCT 2090

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000.

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
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36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2090	100.0	2090	6	AX088250
2	131	6.3	6644	6	E23356
3	131	6.3	7372	6	E23357
4	131	6.3	7797	6	E23355
5	131	6.3	7996	6	E23359
6	129.6	6.2	840	8	CMS0180K
7	129	6.2	213530	2	AC090493
8	128	6.1	160788	2	AC090493
9	127	6.1	160788	2	AL592166
10	126.4	6.0	14867	2	AE001398
11	123.2	5.9	217930	2	AC026471
12	122.6	5.9	99003	2	AL390756
13	121.6	5.8	1496	3	CEY53C12D
14	121.6	5.8	67970	3	PFMAL1P3
15	121.6	5.8	253305	3	PFMAL1P3
16	120.4	5.8	4601	3	DMU11584
17	120.4	5.8	19517	3	DMU37541
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20	120	5.7	169546	2	AC004157
21	119	5.7	201312	2	AC067900
22	118.6	5.7	183584	2	AC012492
23	118.6	5.7	303091	2	AC084799
24	118	5.6	159354	2	AL391425
25	118	5.6	326924	2	AC093082
26	117.4	5.6	172631	2	AC012566
27	117.2	5.6	137889	2	AC073269
28	117	5.6	50612	9	AL513350
29	116	5.6	44352	3	AE098501
30	116	5.6	143585	2	AC013349
31	115.2	5.5	124057	9	AP000770
32	114.6	5.5	126999	9	AL513328
33	114.2	5.5	54345	2	AC084152
34	114	5.5	114897	2	AP003624
35	114	5.5	298469	3	AE003846
36	113.2	5.4	1707	3	AF388909
37	113.2	5.4	2426	8	SDU49822
38	112.6	5.4	66441	2	PFMAL1P4
39	111.8	5.3	179902	2	AP003630
40	111.8	5.3	194212	2	AC092148
41	111.6	5.3	65691	3	PFMAL1P1
42	111.4	5.3	156550	2	AC015830
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ALIGNMENTS

RESULT 1
LOCUS AX088250 2090 bp DNA
DEFINITION Sequence 1 from Patent WO0114572.
ACCESSION AX088250
VERSION AX088250.1 GI:13397159
KEYWORDS
SOURCE
ORGANISM

Beta vulgaris.
Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.

REFERENCE
1 (bases 1 to 2090)
Duvenig, E. and Rausch, T.

TITLE
Autors
Plant gene expression, controlled by constitutive plant v-atpase promoters
JOURNAL
Patent: WO 0114572-A 1 01-MAR-2001;
BASF AKTIENGESellschaft (DE)

FEATURES
source
1..2090
Location/Qualifiers

/organism="Beta vulgaris"
 /db_xref="taxon:161934"
 /note="Promotor subunit c isoform 2"
 1..1923
 BASE COUNT 794 a 354 c 271 g 671 t
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 6.3e-258;
 Matches 2090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 AACTTCGAAGTATTCATTCATTCGACCTTATGATGTAAGTGAAGAAATGAGATATA 120
 DB 61 AACTTCGAAGTATTCATTCATTCGACCTTATGATGTAAGTGAAGAAATGAGATATA 120
 QY 121 GGAATAGTGAAGAGGCTTTATATTAATTAAGCTTAATTAATTTGATTCATTTATAT 180
 DB 121 GGAATAGTGAAGAGGCTTTATATTAATTAAGCTTAATTAATTTGATTCATTTATAT 180
 QY 181 CTGAAAACAAGTATGATGAATTTGATTCATTTATGACACGATGAGAAAGTTAAGA 240
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 QY 241 TTTAGTCTTTTAAATTTCCATATTAATTTTGGCCCAACCTTTTGCATAATATC 300
 DB 241 TTTAGTCTTTTAAATTTCCATATTAATTTTGGCCCAACCTTTTGCATAATATC 300
 QY 301 CATGTCGGAATTAATTTGAAAAACAACAATATCAACCTTTTGGCAACAATTT 360
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 QY 361 TACAAAATTCATTCGAAAAAAATTTACATTAACCTGGAATCAAAATTTGTAT 420
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 QY 421 GAAAAATTTAAATTTCTTCCACCTAATTAATGAACTCAAGGTTAAATTTAGAAAA 480
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 QY 481 GGAGAAAAATTAATAATGACCATTTTCATGGAATCAAAATTTGTATGAAAACTTAAA 540
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 DB 601 AATGACATTTTCATTCAAAATCAGATTTGTATGAAAAATTTAAATTTTATTTCAATA 660
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 DB 721 GTAAACATTCATTTGTAATTCAGAAATTTAGAAATTTAGAACAGAAAAATTCGAAAT 780
 QY 781 GTCTTATCTTTGCGTTACAAATTTTGGATCATTAAGAAATTTCTGAAATCCATATCA 840
 DB 781 GTCTTATCTTTGCGTTACAAATTTTGGATCATTAAGAAATTTCTGAAATCCATATCA 840
 QY 841 AAACATTAATTAATTAACAAAATGAAATTAACCAAAAAAGAACATGACATATTTTC 900
 DB 841 AAACATTAATTAATTAACAAAATGAAATTAACCAAAAAAGAACATGACATATTTTC 900
 QY 901 GTAAAGAACATCATCTAGTATATAAAGAACATGCGCATATTTAGAAATTTGAAAAA 960

DB 901 GTAAAGAACATCATCTAGTATATAAAGAACATGCGCATATTTAGAAATTTGAAAAA 960
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 DB 1321 AATGAGGAAAAACTGTTTCTCTATCTCTCTGTGACATTTCTGACATGACCTTAC 1380
 QY 1381 TTTCCCTTTTATTTACTCTTCAATTTCTTCTTGTGATGAAACCAACAACGGA 1440
 DB 1381 TTTCCCTTTTATTTACTCTTCAATTTCTTCTTGTGATGAAACCAACAACGGA 1440
 QY 1441 ACTAATTTTGAATTTGTTTCCATTTGTAATTTTTCATGAAATTCATTTTAACCT 1500
 DB 1441 ACTAATTTTGAATTTGTTTCCATTTGTAATTTTTCATGAAATTCATTTTAACCT 1500
 QY 1501 GAAATTTTGAATTTGTTTCCATTTGTAATTTTTCATGAAATTCATTTTAACCT 1560
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 QY 1561 CAAATTTGCAATTTGTTTACCTTTCTTAATTTGTTTCAATTTGTTTCAATTTGTTT 1620
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 QY 1681 AAAAGTCCACAGCCCAATTTAGGCTCCCAAAACACGAAATTTCTGTAATTT 1740
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 QY 1861 AAAAATTAATAATAAAGAAAGATTAATTAATTAATTAATTAATTTGCTCTATATC 1920
 DB 1861 AAAAATTAATAATAAAGAAAGATTAATTAATTAATTAATTAATTTGCTCTATATC 1920
 QY 1921 CTCATATTTTCAATTCACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
 DB 1921 CTCATATTTTCAATTCACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
 QY 1981 TCGATCAACGCAATTCATGAAACACCTTCCGATCATCACATCAAAAAATTTGTAAG 2040

Db 1981 TCGGATCAAGCAATTCATCGAACACCTTCGATCATCACCATCAAAAAATGTCAACAG 2040
 QY 2041 TCTTAAAGCGATGAAGCGCCGCTTCTGGCTTCTGGCGTCTG 2090
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RESULT 2
 E23356 6644 bp DNA PAT 07-FEB-2001
 LOCUS E23356
 DEFINITION Virus vector system expressing apoptosis-related gene.
 ACCESSION E23356.1 GI:13024379
 VERSION JP 199075859-A/2.
 KEYWORDS Unidentified.
 SOURCE Unidentified.
 ORGANISM Unidentified.
 REFERENCE 1 (bases 1 to 6644)
 AUTHORS Hirofumi, H.
 TITLE Virus vector system expressing apoptosis-related gene
 JOURNAL Patent: JP 199075859-A 2 23-MAR-1999;
 R B R JENSEN KK
 COMMENT OS Unidentified
 PN JP 199075859-A/2
 PD 23-MAR-1999
 PF 08-SEP-1997 JP 1997259235
 PR

PC C12N15/09, C12N5/10, C12N7/00//A61K35/76, A61K48/00, (C12N5/10, PC
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 PC (C12N7/00, C12N1/92), C12N15/00, C12N5/00, (C12N5/00, C12N1/91) CC
 Strandedness: Double;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT source 1.6644
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 /organism="Unidentified"
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 BASE COUNT 2166 a 1573 c 1424 g 1481 t
 ORIGIN

Query Match 6.3%; Score 131; DB 6; Length 6644;
 Best Local Similarity 49.3%; Pred. No. 2.9e-08;
 Matches 341; Conservative 0; Mismatches 350; Indels 0; Gaps 0;

QY 322 AAAAAACAATATCAATCTTTTGGCAACAATTTTCAAAAAATCCATTTTCAGAA 381
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 QY 442 CACCTATATGAACTCAAGCTTAAATTTGAAAAAGAGAAAAATTAATATGACC 501
 Db 3861 AAAAAATTTTACATTAACCTTGGCAATCAATTTGTATGAAAAATTTAAATTTCTTT 441
 QY 502 ATTTCATCGAATCAATTTGTATGAAAAATTTTAAATTTTAAATTTAAATTTGA 561
 Db 3921 AAAAAATTTTACATTAACCTTGGCAATCAATTTGTATGAAAAATTTAAATTTCTTT 441
 QY 562 AATTCAGATGTTAAATTTGAAAAAGAGAAAAATTTAAATTTGACCTTTTCATTCAGAA 621
 Db 3981 AAAAAATTTTACATTAACCTTGGCAATCAATTTGTATGAAAAATTTAAATTTCTTT 441
 QY 622 CAGATTTGTATGAAAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTGA 681
 Db 4041 AAAAAATTTTACATTAACCTTGGCAATCAATTTGTATGAAAAATTTAAATTTCTTT 441
 QY 682 ACATTTAGAAAAAGAAAAATTTAAATTTGATGAAAAATTTTAAATTTTAAATTTTGA 741

Db 4101 AAAAAACAATATCAATCTTTTGGCAACAATTTTCAAAAAATCCATTTTCAGAA 4160
 QY 742 TCGAATTTAGAGAGTTAGCAAGAAAAAAATCTGATTTGTACTTTTGGTTCACA 801
 Db 4161 AAAAAACAATATCAATCTTTTGGCAACAATTTTCAAAAAATCCATTTTCAGAA 4220
 QY 802 ATTTGGATCAATTAAGAAATTTCTGAATTCATTCATTAATTTTAAATTTCAAAA 861
 Db 4221 AAAAAACAATATCAATCTTTTGGCAACAATTTTCAAAAAATCCATTTTCAGAA 4280
 QY 862 ATGCAATTAACCAAAAAAGAAAGAACATGACGATATTTTGTAAAGACATCATCTGATT 921
 Db 4281 AAAAAACAATATCAATCTTTTGGCAACAATTTTCAAAAAATCCATTTTCAGAA 4340
 QY 922 ATTAAGAACATGCGCATTTTGAATTTGAGAAACAAAAAATCTATTCATTCAGAA 981
 Db 4341 AAAAAACAATATCAATCTTTTGGCAACAATTTTCAAAAAATCCATTTTCAGAA 4400
 QY 982 GGATACACATTCATCAAGAAATGAAAGAAAT 1012
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 LOCUS E23357
 DEFINITION Virus vector system expressing apoptosis-related gene.
 ACCESSION E23357
 VERSION E23357.1 GI:13024380
 KEYWORDS JP 199075859-A/3.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 Hirofumi, H.
 TITLE Virus vector system expressing apoptosis-related gene
 JOURNAL Patent: JP 199075859-A 3 23-MAR-1999;
 R B R JENSEN KK
 COMMENT OS Homo sapiens (human)
 PN JP 199075859-A/3
 PD 23-MAR-1999
 PF 08-SEP-1997 JP 1997259235
 PR

PC C12N15/09, C12N5/10, C12N7/00//A61K35/76, A61K48/00, (C12N5/10, PC
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 PC (C12N7/00, C12N1/92), C12N15/00, C12N5/00, (C12N5/00, C12N1/91) CC
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 FH Key Location/Qualifiers
 FT source 1.7372
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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 ORIGIN

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 Best Local Similarity 49.3%; Pred. No. 2.8e-08;
 Matches 341; Conservative 0; Mismatches 350; Indels 0; Gaps 0;

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Db	4649	AA	4708
OY	562	AATTCAAAGTGTTAAATTTAGAAAAAGCAAAAAATTAAATGCCATTTCATCAAAAT	621
Db	4709	AA	4768
OY	622	CAGATTGTATGAAAAAATTTTAAATTTTATTTCAAAATATATATGAAACTCAAGTGA	681
Db	4769	AA	4828
OY	682	ACATTTAGAAAAAGGAAAAATTTAAATCATGAAAAATTTGTAAAAACATCAATTTTCGAA	741
Db	4829	AA	4888
OY	742	TCAGATTTAGAAAGTTAGACAGAAGAAAAAACTAAATGTCTTACTTTCCGTTCA	801
Db	4889	AA	4948
OY	802	ATTTGGGATCATTAAGAAATTTACTGAAATTCATATCATAAACCTATTTAATTCAAAA	861
Db	4949	AA	5008
OY	862	ATGAATTAACCAAAAAAGAAACATGACGATTTTCGTAAGACATCATCTGATT	921
Db	5009	AA	5068
OY	922	ATTAAGAAACATCGGCATATTAGATTAGAAACAAAAAACTATTCAAATTCACAAAAT	981
Db	5069	AA	5128
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DEFINITION	Virus vector system expressing apoptosis-related gene.	PAT	07-FEB-2001
ACCESSION	E23355		
VERSION	E23355.1	GI:13024378	
KEYWORDS	JP 1999075859-A/1.		
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 7797)		
AUTHORS	Hirofumi,H.		
TITLE	Virus vector system expressing apoptosis-related gene		
JOURNAL	Patent: JP 1999075859-A 1 23-MAR-1999;		
COMMENT	R B R JENSEN KK OS Bovine poxvirus PN JP 1999075859-A/1 PD 23-MAR-1999 PF 08-SEP-1997 JP 1997259235 PR		
PI	HIROFUMI HAMADA		
PC	C12N15/09,C12N5/10,C12N7/00/A61K35/76,A61K48/00,(C12N5/10, C12R1:91), PC (C12N7/00,C12R1:92),C12N15/00,C12N5/00,(C12N5/00,C12R1:91) CC Strandedness: Double; Topology: Linear; CC Topology: Linear; FH Key Location/Qualifiers FT source 1..7797 FT /organism='Bovine poxvirus'. FT Location/Qualifiers 1..7797		
FEATURES			
source	Location/Qualifiers 1..7797		

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Best Local Similarity	49.3%	Pred. NO. 2.8e-08			
Matches 341	Conservative	0	Mismatches 350	Indels 0	Gaps 0
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QY	442	CACCTTAATTTGAACCTCAAGTGTTAAATTTAGAAAAGGAGAAAATTAATAATGACC	501		
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QY	502	ATTTCATCGCAATCAATTTGTATGAAAACCTTAATTTTAAATAATTAATGCA	561		
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QY	562	AATTCAGAGTGTTAAATTTAGAAAAGGAGAAAATTAATAATGACATTCATTCAAAT	621		
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QY	802	ATTTTGGATCAATTAAGAAATTTACGAAATCCATTCAAAACATATTAATTAACAAA	861		
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QY	862	ATGATATTAACCAAAAAGAGAACATGACGATTTTCGTAAGAACATCACTACTGATT	921		
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QY	922	ATAAAGACATGCGCATTTAGAAATGAGAAACAAAACACTATTCAAATTCACAAAAT	981		
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RESULT	5				
LOCUS	E23359	7996 bp	DNA	PAT	07-FEB-2001
DEFINITION	Virus vector system expressing apoptosis-related gene.				
ACCESSION	E23359				
VERSION	E23359.1	GI:13024382			
KEYWORDS	JP_1999075859-A/5.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 7996)				
	Virus vector system expressing apoptosis-related gene				

JOURNAL Patent: JP 1999075859-A 5 23-MAR-1999;
R B R JENSEN KK
OS Homo sapiens (human)
PN JP 1999075859-A/5
PD 23-MAR-1999
PF 08-SEP-1997 JP 1997259235

PC HIROPUMI HAWADA
PC C12N15/09, C12N5/10, C12N7/00//A61K35/76, A61K48/00, (C12N5/10, PC
C12R1:91),
PC (C12N7/00, C12R1:92), C12N15/00, C12N5/00, (C12N5/00, C12R1:91) CC
Strandedness: Double;
CC Topology: Linear;
FH Key
FT source
FT 1.7996
Location/Qualifiers
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FEATURES
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1.7996
Location/Qualifiers
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BASE COUNT 2463 a 2015 c 1829 g 1689 t
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Query Match 6.3%, Score 131, DB 6, Length 7996;
Best Local Similarity 49.3%, Pred. No. 2.8e-08;
Matches 341; Conservative 0; Mismatches 350; Indels 0; Gaps 0;

OY 322 AAAAAACAAACATTCACACCTTTTTCGGAACACCTTTTCACAAATTCATTTTCAGAA 381
DB 5093 AA 5152
OY 382 AAAAAATTTACATTAATTCGGAATTCGTAATTAATTAATTTTCCCTT 441
DB 5153 AA 5212
OY 442 CACCTATATTAAGTCAAACTGTTAAATTTGAAAGAGAGAAATTAATAATGACC 501
DB 5213 AA 5272
OY 502 ATTTCATCGAATCAATTTGTAATGAACCTTAATTTTAAATTAATTAATGA 561
DB 5273 AA 5332
OY 562 AATTCAGTGTAAATTTGAAAGAGAGAAATTAATAATGACCTTCATTCATAAT 621
DB 5333 AA 5392
OY 622 CAGATTTGTATGAATTAATTTTATTTCAATATTAATTAATTAATTAATGA 681
DB 5393 AA 5452
OY 682 ACATTTAGAAAGAGAAATTAATTAATTAATTTGTAATTAATTAATTTGTA 741
DB 5453 AA 5512
OY 742 TCAGATTTGAGACTTGACAGAGAAATTAATTAATTTGCTTATCTTTGCTTACA 801
DB 5513 AA 5572
OY 802 ATTTGGATCATTAAGAAATTTACTGAATCCATCAAAATCAATTAATTAATTA 861
DB 5573 AA 5632
OY 862 ATGATTAACCAAAAGAGAGACATGAGATTTTCGTAAGAGACATCATCTGATT 921
DB 5633 AA 5692
OY 922 ATTAAGAGACATGAGATTTAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 981
DB 5693 AA 5752
OY 982 GGATTAACACATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1012

DB 5753 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAT 5783

RESULT 6
CNS0180K/c
LOCUS
DEFINITION
CNS0180K 840 bp mRNA PIN 02-SEP-1999
Botrytis cinerea strain 74 cDNA library under conditions of
nitrogen deprivation.
ACCESSION
AL110675
VERSION
AL110675.1 GI:5824962
KEYWORDS
cDNA library; nitrogen deprivation.
SOURCE
Botryotinia fuckeliana
ORGANISM
Botryotinia fuckeliana
REFERENCE
1 (bases 1 to 840)
Elkayota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryotinia.
AUTHORS
Bitton, F., Lewis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.
TITLE
Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
78026 Versailles, France
JOURNAL
2 (bases 1 to 840)
Genoscope.
REFERENCE
Direct Submission
Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage;
CP 5706 91057 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
The cDNA library to be analyzed within the framework of this
project was created using a Botrytis cinerea strain which was grown
under conditions of nitrogen deprivation, which is the normal
situation for B. cinerea during its development on its host plant.
The library was produced in an oriented direction, in the pBSII
vector.

FEATURES
source
1.840
Location/Qualifiers
/organism="Botryotinia fuckeliana"
/strain="74"
/db_xref="taxon:40559"
/note="Genoscope sequence ID : W3B091"

BASE COUNT 151 a 23 c 79 g 539 t 48 others
ORIGIN

Query Match 6.2%, Score 129.6, DB 8, Length 840;
Best Local Similarity 47.4%, Pred. No. 5.7e-08;
Matches 334; Conservative 0; Mismatches 367; Indels 3; Gaps 1;

OY 405 AATCAATTTGTATGAACAAATTTTAAATTTCTTCACATATTAATTAATTAATGA 464
DB 835 ATATTAATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 776
OY 465 GTTAAATTTAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 524
DB 775 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 716
OY 525 TATGAACAAATTTTAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 584
DB 715 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 656
OY 585 AAG 644
DB 655 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 596
OY 645 ATTTTATTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 704
DB 595 AA 536
OY 705 AATATGATGAATTTGTAAACATCAATTTGTAATTAATTAATTAATTAATTAATTA 764
DB 535 AATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 476
OY 765 GAAAAAATCAATTTGCTTATCTTTGCTTATCTTTGCTTATCTTTGCTTATCTTTG 824

[illegible]

RESULT	7
AC090493/c	
LOCUS	
DEFINITION	
ACCESSION	AC090493
VERSION	213530 bp
KEYWORDS	DNA
SOURCE	Mus musculus clone RP23-201D19, WORKING DRAFT
	HTG
	25-JUL-2001
	SEQUENCE, 4 unordered
	pieces.
	AC090493
	AC090493.2
	GI:15011687
	HTG, HTGS_PHASE1; HTGS_DRAFT.
	house mouse.

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 213530)	McCombie, W.R., Baker, J. P., Bahret, A., Yang, C., Balija, V., Deedha, N.N., de la Bastide, M., Kait, K., King, L., Kirchoff, K.A., Miller, B., Nascimento, L.U., O'Shaughnessy, A.L., Preston, R.R., Rodríguez, S., Santos, L., Shah, R.S., Spiegel, L.A., Palmer, L., Vil, M.D. and Zutavern, T.	Mouse Genomic Sequence	Unpublished
2 (bases 1 to 213530)	McCombie, W.R.	Direct Submission	Submitted (24-FEB-2001) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
COMMENT	On Jul 25, 2001 this sequence version replaced g1:13122744.		

```

Center: Lila Annenberg Hazen Genome Center, Cold Spring Harbor
Laboratory
Center code: CSHL
Web site: http://www.cshl.org/genseq
Contact: mcomblie@cshl.org
-----
Project Information
Center project name: RP23-201D19
Center Clone name: RP23-201D19
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 100656: contig of 100656 bp in length
* 100657 102023: gap of unknown length
* 102024 172443: contig of 70420 bp in length
* 172444 173810: gap of unknown length
* 173811 210022: contig of 36212 bp in length

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FEATURES	*	210023	211388:	gap of unknown length
source	211389	213530:	contig of 2142 bp in length.	
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		/db_xref="taxon:10090"		
		/clone="RP23-201D9"		
BASE COUNT	54181	a	51263	c
ORIGIN			51850	g
			51971	t
				4225 others

Query Match	6.28;	Score 129;	DB 2;	Length 213530;
Best Local Similarity	45.48;	Pred. No. 3.2e-08;		
Matches 435;	Conservative	0;	Mismatches 512;	Indels 12;
				Gaps 3

Oy	92	ATTTCAGCTGGAAAAATGAGTAATAGCAATTAAGTGGAAAGCGTGTATTAATAT	151
Db	209502	AATATTTATATATAAAATTTTAAATTAATTTTNTATATATATAAAATAATTTNNAAAT	209443
Oy	152	AGACTTAATTTGATTCATTTTCATATATCTGAAACAAGTATGTGAATTTGATTC	211
Db	209442	TNTTAAATATATAAANNAAAAATATATTTTAAATATATAAATATATATATATNACNNAA	209383

212 ATTTATGACACTGATGA AAAAGTTAACGATTTAGTTCTTTTTTTTAA AATCCCAATATAA 271

Dp 209382 NTTTATTAAATTTTAAAANTNANATATAAAATTTAATTAAACCAAAAAATAAANNA 209323

373 AATTTCCTCCAAACCTTTTCGAAATATATCCATGTTGGAATATAAATTGAAAAACCAAAA 331

200263

[illegible][illegible]

Dd 209262 NTAATATTTAAITTTTNTAAAAAAAATAAIIATATACTATATTTTAAATTCGA 209263

392 ACATTACTTGGGAATCAAATGTGTATGAAAAATTAAATTTCCCTTCACCCATAAT 451

Db 209202 ACAAAATAT-----AAAATCTAAACCAACCTATAATATTATTAACTAA 209152

QY 452 TGAACCTCAAAGTGTAAATTTAGAAAGGAGAAATAAAAAATGACCATTTCATGCG 511

Dh 209151 ATAAATTATTTNATAAAAAATTATNAAATAAAAAAAATTTAAAAATATATANCACNN 209092

571

(The following section contains horizontal bars representing redacted information.)

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QY 5/2 G T T A A A A I T T A G A A A A G G A G A A A A A I T A A A A I G A C C H I I I C H I I C A T T A B I C M O N I I S I S I V S I

Db 209031 ANNAATAAATTATAAAA--NANAAATATATTTAAATTAAATANNNAANAATTT 2089/4

632 ATGAAAAATTAAATTTTATTTCAAATATAATTGAACTCAAAGTGTGAACATTAGAA 691

Db 208973 TTATAAAAAACAATTATTTAAAAATNAAANCATATCAANAANTAAAATATTTAAAN 208914

692 AAGGAGAAATTTAAATGATGAATTTGTAACATCAATTTGTGAATCAGAAITTA 751

[illegible]

011

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[illegible]

QY 812 CATAAGAAATTACTGAATCCATATCAAAAACCTATTATTAATTACAAAAAIGAAIAAAA 8/1

Db 208793 TAATAAAATTAATTNTAAAT-AAAATAAAAAAATNAATATAAAAAATATAAATAN 20873

872 CCAAAAAGAGACATGACGATATTTCCGTAAGAACATCATACTGATTATAAAGAAC 931

Db 208734 TATAATNNAAAAAAANTATTATATANTAAAAANAAATTTATAAANTCTANNCANNA 20867

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FEATURES

SOURCE

Dp 65165 AATATATAATATATATAAAATATATAATATATATAAATAATATATACGATTATTTGAACATTA 65106

QY	141	TTTATTAATTAATAGACTTAATTTGATTCATTTTCATATATCTGAAACACAGGTATGATG	200
Db	118612	TATATATTAATATATATATTAATATATTAATATATATTAATATATTAATATATTAATATA	118672
QY	201	AAATTTGATTCATTTTGTGACCTGATGAAAGAAAGTTAAGCATTTTGCTTTT	260
Db	118672	TAAATATATATTAATA	118733
QY	261	TTTCCAAATTAATTTTTTGGCCCAAACTTTTGCAAAATTCATGTCGGAATTAATTTT	320
Db	118732	TAAATATATATTAATA	118793
QY	321	GAAAAACAACAATATCAACCTTTTGGCAGACACTTTTACAAAAATCCATTTTCAGA	380
Db	118792	AATATATTAATA	118851
QY	381	AAAAAAATTTTACATTAAGTCCGAAATCAATGCTG-TATGAAATATTTAAATTTTCT	439
Db	118852	TATTAATAATATATTAACAATATATTAATATATATTAATAATATATTAACAATATATAAATA	118911
QY	440	TTTACCTATTAATTTGAACTCAAAAGTGTAAATTTAGAAAAAGAGAAAAATAAAAATGA	499
Db	118912	AATATATATTAATAATATATTAACAATATATATATATATATATATATATATATATATA	118972
QY	500	CCATTTCAATGCAAAATCAAAATTTGCTATGAAAACTTAATAATTTTAAATATATAT	559
Db	118972	AATATATTAATAATATATTAATAATATATTAATATATATATATATATATATATATATAT	119032
QY	560	GAAATTCAAAGTGTAAATTTAGAAAAAGAGAAAAATTTAAATGACCATTTCAITCAAA	619
Db	119032	ATTAATAATATATATTAACAATATATTAATATATTAATAATATTAACAATATTAATATATA	119092
QY	620	ATCAGATTTGTATGAAAAATTTTAAATTTTATTTTCAATATATATTAATGAACCTCAAAAGTG	679
Db	119092	ATATATTAACAATATATTAATATATTAATATATTAATAATATTAACAATATTAATATATA	119152
QY	680	GAACTTTTGAAGAAAGAGAAAAATTTAAATGATGAAAAATTTGTAAAAACATCAATTTGTGA	739
Db	119152	ATATATATATTAATAATATATTAATAATATTAATAATATTAATAATATATATATATATA	119212
QY	740	AATCAGATTTTGAAGATTTAGACAGAGAAAAAACTGAATTTGCTTATCTTTGCGTTA	799
Db	119212	TATTAATATATATATATATATATTAATATGTTATAA--TATATATTAATAATATAAATATATA	119268
QY	800	CAATTTTGGATTCATTAAGAAATATCTGAATCCATATCAAAAACATATTAATTAACAA	859
Db	119268	AAATATATTAATATATATTAAT	119328
QY	860	AAATGATTAACCAAAAAAGAAAGAACATGAGCATATTTTCTTAAGAACATCACTACTGA	919
Db	119328	AAATATATTAATATATTAATATATTAACAATATTAATATTAATATTAATAATTAACATTAATAAG	119388
QY	920	TTATTAAGAAACATGCGCATATTTAGATTTGAGAAACAAAACTATTCAAAATCACAAA	979
Db	119388	ATATATTAAGATTAATAAGATATTAATTAATTAATTAATTAATAATTAATAATATATATA	119448
QY	980	ATGATTAACAACATACATCAAAAGACATGAAAGAACTTATTCACAAAATGAGAGTGAACCTTA	1039
Db	119448	AGATATTAATTAATATATTAAGATATATTAATATATTAAGATATATTAATATTAATATATA	119508
QY	1040	AATTTCTACTGTCATTTTTCAGTTTATTTTACTACTAGTATTAAGCGCTAAATAAT	1094
Db	119508	TATATTAAGATATATTAATATATATATATTAATAATATTAATAATATATTAATAAATAT	119563

RESULT 10

AE001398/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

AE001398

14867 bp

DNA

Plasmidium falciiparum chromosome 2, section 35 of the complete sequence.

AE001398 AE001362

AE001398.1 GI:3845197

INV

06-NOV-1998

SOURCE	REFERENCE	TITLE	JOURNAL	MEDLINE	REMARK	FEATURES	GENE	CDS	BASE COUNT
ORGANISM	malaria parasite P. falciparum								6284
REFERENCE	1 (bases 1 to 14867)								a
AUTHORS	Gardner,M.J., Tetteh,I.H., Carucci,D.J., Cummings,L.M., Arayind,L., Koolin,E.V., Shallow,S., Mason,T., Yu,K., Fujii,C., Pederson,J., Shen,K., Jing,J., Aston,C., Lai,Z., Schwartz,D.C., Pettee,M., Salberg,S., Zhou,L., Sutton,G.G., Clayton,R., White,O., Smith,H.O., Fraser,C.M., Hoffman,S.L. et.al.								
TITLE	Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum								
JOURNAL	Science 282 (5391), 1126-1132 (1998)								
MEDLINE	99021743								
REMARK	Erratum:[[published erratum appears in Science 1998 Dec 4;282(3395):1827]]								
REFERENCE	2 (bases 1 to 14867)								
AUTHORS	Gardner,M.J.								
TITLE	Direct Submission								
JOURNAL	Submitted (02-NOV-1998) The Institute for Genomic Research, 9712 Medical Center Drive, Rockville, MD 20814, USA								
FEATURES	Location/Qualifiers								
SOURCE	1..14867								
GENE	/organism="Plasmodium falciparum"								
CDS	/db_xref="taxon:5833"								
GENE	/chromosome="2"								
CDS	complement(1570..2424)								
GENE	/gene="PF80490c"								
CDS	complement(1570..2424)								
GENE	/gene="PF80490c"								
CDS	/note="predicted by Glimmer"								
GENE	/codon_start=1								
CDS	/product="hypothetical protein"								
GENE	/protein_id="AAC71887.1"								
CDS	/db_xref="gi:3845198"								
GENE	/translation="MKEKNEIMDYLSCPIDDDVYDRKKSGKSNILKSSSTKSDYKK								
CDS	SIPTSKRDSHKSGSPGRSGEINRSGSEFKPPYNNRLINNNYGNPHNHR								
GENE	DNEGRTGSCGSRPFDRKSGSEFKRPIISNRKSSVKSIRGSKMKGKSFNPATSR								
CDS	TVYKRLNNKTVASAPVKKENNNLISYLRNRFALTNRKPGVITKSSVPKRIKK								
GENE	GLKGSLSKSTKSTSGSKPKLKKPLKIKITVTSILNKIPSPLEQNTPEVNPEST								
CDS	NNATTKN"								
GENE	11241..14606								
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CDS	/codon_start=1								
GENE	/product="hypothetical protein"								
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GENE	/db_xref="gi:3845199"								
CDS	/translation="MFALKRNVREGFVNICFSYLKLYLKSNEVTVNLNVEETNNEKR								
GENE	TNRKYRSKAQSLFEDGLIMHKLILFKMLPYKCAKYECSIAKEVYKLLDEYKGC								
CDS	FNYSILDIOSVATPEDELDTFTFDYVLEVNIDKVNLIKINETFKKDLTPHRR								
GENE	ELIIGLCKINIKSYIHEMNGELIHLFIPPRMKNDKNIILFYVFNYPYFDMYLFN								
CDS	HEIKLFIENKYLNNNSNIPFNKNILOEMFNLYFRELKNEKNTITKNNKEIYRK								
GENE	CAKHEFNVDINERKFLNLRILVYDNSIIDDINNMKLNNNNLINENIEYISKL								
CDS	MFCTILKRSKIDNDMTYKLEVIKATHNLLDCKKNIETPCSDIDYSLFSLSNLK								
GENE	FLNKLIDKNFLEVECLIKILINIKENAVQSCISLSLKNYILNRNRYIVNRY								
CDS	LFDIMKFSLYLNICIEFKRITENENAVLIINMOTNYSNENIKDIIIOKRIEY								
GENE	ILFKEMENYKDFEFLKSDSLSTIKLSNPEPVKINENYSDFYLLFNISICLYNLY								
CDS	NRSVSKRDYTIYIILNDSFYKIKNDRTRKKNFLLSSMKELICKNLLYSN								
GENE	RYIKHAEEDNPDOKDOYVSLFNLNLPDKTIIFHYIYINLMCHVYKTYNFKCNKL								
CDS	INEDYISLLLTSCFOYFLENNSDRYCKEKLHLKYNLIIDILIKNYYLNATYSID								
GENE	NISKIFISLNSKYTCVEYNLNLLESIOSFEVYTSKGGIHAMNDNLDNNSCE								
CDS	KYHRYIEYKKNLFIINLIKILINIKENAVQSCISLSLKNYILNRNRYIVNRY								
GENE	KLIYLIANNLYENMYGCEMLERVLSSKEQNLFSYNNKNEVHEKMDKILCHSE								
CDS	DDYIEMSNMYVLYFYDIKINNSEROSNIIIRNSSTDRPIDEIKKKYILNNNTLKH								
GENE	NNKYNLEKSNNSNGNINSLKDKKNKNHNMEDLIDKNENKRIQEGONGEEN								

OY 132 AAAAGGCGTTTATATAATTAGACTAAATTTGATTCANTTTCATATCTGAAAAACAG 191
 ||| | | | | | | | | | | | | | | | | | | |
Db 25297 AATNTTTTTTAATATATAATATAAATAAAAAAAAAAAAAAAAAATAAATAATAT 25350

RESULT	12
LOCUS	AL390756/c
DEFINITION	AL390756 99003 bp DNA HTG 13-JUN-2001
ACCESSION	Homo sapiens chromosome 1 clone RP11-378A4, *** SEQUENCING IN PROGRESS ***, 29 unordered pieces.
VERSION	AL390756
KEYWORDS	AL390756.2 GI:9931005
SOURCE	HTG: HTGS_PHASE1; HTGS_CANCELLED. human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 99003)
AUTHORS	Mclay,K
TITLE	Direct Submission


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misc_feature      57706..60028
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misc_feature      60129..63554
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misc_feature      72915..78995
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misc_feature      82653..85473
/Note="assembly-fragment:00752"
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/Note="assembly-fragment:00834"
misc_feature      88179..90954
/Note="assembly-fragment:00887"
misc_feature      91055..95382
/Note="assembly-fragment:00939"
misc_feature      95483..99003
/Note="assembly-fragment:01026"
BASE COUNT      24057 a 23751 c 23770 g 24578 t 2847 others
ORIGIN

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Query Match      5.9% Score 122.6; DB 2; Length 99003;
Best Local Similarity 48.6%; Pred. No. 2.3e-07;
Matches 368; Conservative 0; Mismatches 385; Indels 4; Gaps 2;

QY 194 ATGTATGAAATTTGATTCATTTATGACACGTGTAAGAAAGTAAAGCATTTGCTCTTTT 253
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QY 254 TTTAAATTCAGATTAATTTTGGCCCAAACTTTGGCAAAATATCCATGTCGAAAT 313
DB 11028 TANTATATAGTAAATTTCAAAATFANANATTAATTAATTAATTAATTAATTTTATA 10969
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QY 434 TTTCTTCCACCTATATATGAACTCAAGTGTAAATTTAGAAAAGAGAAAAATATA 493
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QY 732 ATTTGTGAATTCAGATTTGAGAGTTAGACAGAAAAAATGGAATTTCTTAACTT 791
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QY 792 TTGCGTTACATTTTGGATCATAGAAATTTACTGAATCCATATCAAAACATATATA 851
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RESULT 13
CEY53C12D/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REMARK
REFERENCE
AUTHORS
TITLE
JOURNAL

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Genome sequence of the nematode *C. elegans*: a platform for investigating biology. The *C. elegans* Sequencing Consortium Science 282 (5396), 2012-2018 (1996)

Submitted (02-NOV-1998) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1HQ, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jess@wustl.edu

Current sequence finishing criteria for the *C. elegans* genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone Y53C12D. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The start of this sequence (1..117) overlaps with the end of sequence 299277.

The end of this sequence (1390..1496) overlaps with the start of sequence 299278.

For a graphical representation of this sequence and its analysis see: <http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=Y53C12D>.

FEATURES

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ORIGIN

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Matches 481; Conservative 0; Mismatches 519; Indels 8; Gaps 4;

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[illegible]

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 MOULE, S., MUNAGAL, K., MURPHY, L., OLIVER, K., QUAIL, M.A.,
 RAJANDREAM, M.A., RUTER, S., SKELTON, J., SQUARES, R., SQUARES, S.,
 SULSTON, J.E., WHITEHEAD, S., WOODWARD, J.R., NEWBOLD, C. and
 BARRELL, B.G.
 The complete nucleotide sequence of chromosome 3 of *Plasmodium
 falciparum*
Nature 400 (6744), 532-538 (1999)
 2 (bases 1 to 253305)
 Oliver, K., Bowman, S., Harris, D., Lawson, D., Quail, M. and Barrell, B.
 Unpublished
 3 (bases 1 to 253305)
 Lawson, D., Bowman, S. and Barrell, B.
 Direct Submission
 submitted (17-DEC-1998) *P. falciparum* Genome Sequencing Consortium.
 The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
 CB10 1SA, UK
 On May 14, 2001 this sequence version replaced gi:2982540
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 For more information about this sequence or the Malaria Project,
 see http://www.sanger.ac.uk/Projects/P_falciparum.
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Query Match
Best Local Similarity 5.8%; Score 121.6; Db 3; Length 253305;
Matches 444; Conservative 0; Mismatches 484; Indels 12; Gaps 2;

141 TTTATATTAATTGACCTTAATTTGATTCATTTTCAATATCTGAAACAGATGATG 200
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DB 222931 TTTTATATTTTGAAGCTAATATATATAGTGATATATATATATATGTTTGTG 222872

201 AATTTGATTCATTTATGACCTGATGAAAGTAAACAGATTTATCTTTTATAAA 260
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DB 222871 TATATGATGCTGCTGATGATGTTGATATATATATGATATATATATATAT 222812

261 TTCCATATTAATTTTGGCCAAACCTTTGGCAATATCATGTTCCGAATATAATTT 320
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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381 AAAAAAATTTTACATTAACCTTGC-----AATCAAAATTTGATGAAAAATTTAA 431
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DB 222691 AAAAAATTTTAAATATATATATATATATATATATATATATATATATATAT 222632

432 AATTTCCCTTTCACCTATATATGAAGCTGTTAAATTTAGAAAAGAGAAAAATA 491
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DB 222631 TGAATAAATATATATCAAAAAAATTAATAAAAAAATTTATATATAAACAATGATATA 222572

492 AAAAAATGACATTCATGCGAAGTAAATTTGATGAAAAACTTAAATTTTATTTTAA 551
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DB 222571 AAAAAAATTTTATACATATAAAAAAGAAAAAAGAAAAAAGAAAAAATATATA 222512

552 ATATATATGAATTCAGATTTAAATTTAGAAAAGAGAAAAATTAATTAAGCAATTT 611
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DB 222511 TCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 222452

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[illegible]

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Search completed: February 23, 2002, 08:50:12
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2002, 06:33:03 ; Search time 121.84 Seconds
(without alignments)
14706.252 Million cell updates/sec

Title: US-09-636-826-1

Perfect score: 2090
Sequence: 1 GATATCACACATTCGTCAT.....TCGCTTCTGCTGCTGCT 2090

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	266	12.7	936	22	AAAF58262
7	266	12.7	936	22	AAAF58255
8	264.6	12.7	936	22	AAAF58252
9	264.6	12.7	936	22	AAAF58254
10	264.6	12.7	936	22	AAAF58257
11	264.6	12.7	936	22	AAAF58259

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13	264.6	12.7	938	22	AAAF58255	Oligonucleotide D1
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15	131	6.3	7372	20	AAAX33182	Base sequence of t
16	131	6.3	7797	20	AAAX33180	Base sequence of t
17	131	6.3	7996	20	AAAX33184	Base sequence of t
18	105.4	5.0	1035	21	AAAO1936	Human colon cancer
19	101	4.8	9789	17	AAAT41852	CDNA encoding plas
20	97	4.6	19124	18	AAAT2882	Plasmodium var-7 g
21	97	4.6	19124	21	AAAZ98287	Plasmodium var-7 p
22	91.4	4.4	6033	21	AAAT70152	Plasmodium falcipa
23	89.6	4.3	335913	22	AAI61371	Soybean 240017 reg
24	89.6	4.3	335913	22	AAI61372	Soybean 240017 reg
25	88	4.2	875	21	AAAO1920	Human colon cancer
26	87.6	4.2	6042	21	AAAT70199	Plasmodium falcipa
27	86.8	4.2	8310	20	AAAZ29911	CDNA encoding a SC
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29	86.2	4.1	2503	15	AAO53480	P. falciparum telo
30	85.2	4.1	4041	21	AAAT70170	Plasmodium falcipa
31	84.4	4.0	244	22	AAAF58238	Plasmodium falcipa
32	84	4.0	1132	21	AAAF12929	Oligonucleotide D1
33	83.4	4.0	244	22	AAAF58238	Oligonucleotide D1
34	82.8	4.0	1527	21	AAAT70121	Plasmodium falcipa
35	81.6	3.9	26811	20	AAAX20253	Plasmodium falcipa
36	80.2	3.8	700	22	AAH93026	Borrelia burgdorferi
37	79.2	3.8	20674	21	AAAF58017	Human inflammatory
38	79	3.8	11309	20	AAAO20250	Arachidonic acid m
39	78.8	3.8	3101	11	AAAO20247	Borrelia burgdorferi
40	78.8	3.8	5139	21	AAAT70139	Sequence encoding
41	78.4	3.8	1612	7	AAAN60392	Plasmodium falcipa
42	78	3.7	910715	20	AAAZ20248	Sequence encoding
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44	77.4	3.7	5454	21	AAAT70236	Plasmodium falcipa
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ALIGNMENTS

RESULT 1

AAAF61197 standard; DNA; 2090 BP.

AC AAF61197;

23-MAR-2001 (first entry)

B. vulgaris V-ATPase subunit C isoform 2 promoter DNA.

Promoter: V-ATPase; subunit C; isoform 2; plant; transgenic plant;

KW herbicide resistance; disease resistance; insect resistance;

KW nutrient deficiency; injury; infection; selection marker; ss.

OS Beta vulgaris.

PN WO200114572-A2.

PD 01-MAR-2001.

PF 10-AUG-2000; 2000WO-EP07774.

PR 26-AUG-1999; 99DE-1040648.

PR 26-AUG-1999; 99US-0150887.

PA (BAD) BASF AG.

PI Duvenig E, Rausch T;

XX WPI: 2001-218455/22.

XX New DNA construct containing a plant V-type adenosine triphosphatase

PT promoter, useful for recombinant protein expression or producing

PT stress-resistant plants -
 XX
 PS Claim 6: Page 65-66; 69pp; German.
 XX

CC This invention describes a novel DNA construct (I) which comprises a
 CC plant V-ATPase (V-type adenosine triphosphatase) promoter (P), or its
 CC functional equivalent, coupled to a heterologous gene. The invention also
 CC describes (1) a polynucleotide (III) containing the sequence of (P) from
 CC the Beta vulgaris V-ATPase subunit c isoform 2 (2090 bp sequence (1),
 CC reproduced), or its functional equivalents; (2) a recombinant vector
 CC containing (I); (3) a microorganism transformed with the vector of (2);
 CC (4) a transgenic plant cell or protoplast that contains (I); (5) a
 CC transgenic plant containing (I) in its genome; (6) controlling (M1)
 CC expression of (II) in a plant cell or protoplast by transforming with (I)
 CC then exposing to an (a)biotic stress that controls expression of (II);
 CC (7) method (M2) similar to (M1), but applied to regenerated transgenic
 CC plants; (8) preparation (M3) of recombinant proteins (IV) by methods (M1)
 CC and (M2); (9) (III) produced by method (M3); and (10) plant cells or
 CC protoplasts, and regenerated plants, transformed with (I) and resistant
 CC to (a)biotic stresses. (1), and (II) are used to direct expression of
 CC recombinant proteins in plants, or their cells or protoplasts. (III) is
 CC used to provide expression of genes in plants under (a)biotic stresses,
 CC such as genes that impart resistance to insects, herbicides, diseases, or
 CC selection genes. (IV) is used to produce plants with increased resistance
 CC to stress (especially salt but also nutrient deficiency, injury,
 CC infection, presence of herbicides). P are very strong, constitutive
 CC promoters, effective in all parts of a plant, and they become more
 CC active, or are not repressed, under conditions of stress, so are better
 CC than known plant or viral promoters for expressing selection markers and
 CC resistance genes.
 CC
 XX
 SQ Sequence 2090 BP; 794 A; 354 C; 271 G; 671 T; 0 other;

Query Match 100.0%; Score 2090; DB 22; Length 2090;
 Best Local Similarity 100.0%; Pred. No. 1.2e-302;
 Matches 2090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATATCATCATTCGTCATCGACGATTTGCGAATTTTCAATAGTAGTAATCTTTT 60
 DB 1 gatacacatcgcgcacgacgalttgcgaacttccaatagagcgaatcttctt 60
 QY AATCTGAAGATTATTCACATTCAGTACGACATTTATGATGATGAAAAAGAGATATA 120
 DB 61 aatctcaaaagtatctacatctagctactatagtgctgaaaaaagsgaataa 120
 QY 121 GGAATAGTTGAAAAAGGCTTTATATATATTAATTAAGACTTAATTTGATTCATATAT 180
 DB 121 ggaattagttgaaaaggctttatataatagacttaattgattcatttccatata 180
 QY 181 CTGAAAACAGATATGTAATGTAATTCATTTATGACATGAGATGAAAAAGTTAGCA 240
 DB 181 ctgaaaacagatgtaataatgtaattcatctacacgacgaaagaaagtaagca 240
 QY 241 TTTGTTCTTTTAAAAATTCATATATATATTTTGGCCAAAACCTTTGCAAAATATC 300
 DB 241 ttgtgtctttttaaataatccaataataatlttggccaaaactlttgcaaaatc 300
 QY 301 CATGTTGGAATTAATTTTGAACAAACAAATATCAACCTTTTGGCAACACTTT 360
 DB 301 catgttcgaaataaatttgaaaaaaacaacaaatcctlttgcgaacaactlt 360
 QY 361 TACAAAATCCATTTTCGAAAAAAAATTTTACATTAACCTGGGAATTCAAATTTGTAT 420
 DB 361 tacaataatccatttcagaaaaaaataatcaatcaatctgcgaatacctatgtat 420
 QY 421 GAAAAATTTAAATTTCTTTCACCTTAATTAATGAAACTCAAGTGTAAAAATTTAGAAA 480
 DB 421 gaaaatattaaatttcttccacttaattgaaactcaagtgtaaaaaattagaaa 480
 QY 481 GGAGAAAAATTAATAATGACCATTTTCATGCGAAATCAAAATTTGTATGAAAAATTAAAA 540
 DB 481 ggagaaaaataataatgacatttcacgtgaaatacaaatgtgtgtaaaaaacttaaa 540

QY 541 TTTTATTTTAAATATATATGAAATTCAAAGCTTTAAAAATTTAGAAAAAGCAAAAAATTAA 600
 DB 541 tttaatttaataataatgaaatccaagtgtaaaaaattagaaaaagsgaaaaattaa 600
 QY 601 AATGACCATTTTCATTCAAAATTCAGATGTGTATGAAAAAATTTAAATTTTATTTCAATTA 660
 DB 601 aatgacatttcattccaataacagatctgtaaaaaattcaatttatttcaataa 660
 QY 661 TAAATGAAACTCAAGAGTGTGACATTTTGAAGAAAAAGAAAAAATTTAAATGATGAAAAATTT 720
 DB 661 taattgaacaccgaagtgtagacatttagaaaagsgaaaaaataatgatgaaattt 720
 QY 721 GTAAAAACATCATTTTGTGAATTCGAATTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGA 780
 DB 721 gtaaaaacatcattgtgaaatcagaatttagaaggttagacaagaaaaaaactgaa 780
 QY 781 GTCCTTATCTTTGCGTTACAAATTTTGGATCATTAAGAAATTTTCAATTCATTA 840
 DB 781 gtcttatacttlttgggttacatlttgggtacataaagaataatctgaaatccatca 840
 QY 841 AAACATTTATTAATTTACAAAAATGAAATTAACCAAAAAAGAGACATGACATTTTC 900
 DB 841 aaactattataattcaaaaaatgataaaaaaccaaagaagaacatgacgatatltc 900
 QY 901 GTAAAGACATCATTCATGATTTTAAAGAACATGCGATTTTGAATTTGAAAGCAAAAA 960
 DB 901 gtaagaacatcatcactgattatataaagaacaatgcacatattagaaatgaaacaaa 960
 QY 961 ACTATTCAAAATTCACAAAAATGAGTAAACATCATCAAGCAATGAAAGAAATCTTATTTCA 1020
 DB 961 actattcaaaatccaanaaatgataaacaacatacaagaacatgaaagatcttattca 1020
 QY 1021 CAAAATGAGAGTGAACCTTAATTAATTAATTAATTTTCACTTTTCACTTTTCACTTTT 1080
 DB 1021 caaaatgaggtgaaacttaaaactaaacttgcatttcaatttcaacttaactagat 1080
 QY 1081 AGGCTTAAATATCATGACGACGATCGTGCACAAAGAACTAGTTAATGATTCACAA 1140
 DB 1081 aggcctaaatatacatcatcgcacgcacatgcgcacaaagaactagtgtaagatcaca 1140
 QY 1141 GTACAAACATCAACATGATTTTCAATTTAGGCTCCATTTTGTAGGCGTAAACGTTTTC 1200
 DB 1141 gtcaaaaactcaacaactgatttcaatttagagctccattttagggcgttaaaagctt 1200
 QY 1201 CCGGAACACTATTTTTCCTCAATTTTATTTTACATTTTGTGTTGTTGTTGTTGTTGTTG 1260
 DB 1201 ccggaacactatlttcccaatltttagcttcaatltgtgtgtaaaaagagtgtaa 1260
 QY 1261 AACCGTTTCCCTGGGTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320
 DB 1261 aacgcttcccttgggtgtaaaatcttcaatcttcccaatltgtgaaacatttcc 1320
 QY 1321 AATGAAGGAAACGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1380
 DB 1321 aatgaaggaaacgcttcttcccttcttcttcttcttcttcttcttcttcttctt 1380
 QY 1381 TTTCCCTTATTTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1440
 DB 1381 ttcccttatttacttcttcttcttcttcttcttcttcttcttcttcttcttctt 1440
 QY 1441 ACTAATTTTGAATTTGTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1500
 DB 1441 actaatlttggatgtgttcttccatgttaaatgttcttccatgaaatcttctt 1500
 QY 1501 GAAATGTTTTCACCCATCAACAAAGAGCTTGTGTGTCATGAATGATGACGAGTTT 1560
 DB 1501 gaaatgttttacccttaccacaaagagccttgcgtgtgcacatgaatgacagat 1560
 QY 1561 CAAATTCGAAATGAGTTTACGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1620
 DB 1561 caaatcgaaactgggttaccgttcttcttcttcttcttcttcttcttcttctt 1620

Qy 1621 AACTATGTTGCTACCCCTTAAGATGATATGTAATAAACCCTTGAGTGGCTTTGGCTATA 1680
 Db 1621 aactatgttgcctaccccttaagatgatatgttaaaccttcagtggtgcttggctataa 1680
 Qy 1681 AAAAGTCCCAACCAAGCCCAATTTAGTGTCCCAAAACCAAGCAAAATTTCTGTTACTATT 1740
 Db 1681 aaaagtcaccaacagcccaattctagctcccaaacacgaatttctctgactatt 1740
 Qy 1741 CCAAAACAAAACAAACACCTCTGTATCAACCAAGAAAATTAATTAATTTGTTT 1800
 Db 1741 ccaaaacaaaacaaacacccctctgtatcaaacagaaaaataaacatatttctgttt 1800
 Qy 1801 CTCCTCAATTTTCAATTTTATTTATTCACGGAAGATACATTAATTAATCAAGGTA 1860
 Db 1801 ctcccaatttctatttatttattatcaagggaaagtaacaaatcaatcaagggta 1860
 Qy 1861 AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1920
 Db 1861 aaaaaataaataaataaataaataaataaataaataaataaataaataaataaataaata 1920
 Qy 1921 CTCATATTTTCATCAACGCT 1980
 Db 1921 cctcatatttcatcaccgctc 1980
 Qy 1981 TCGATCAAGCAATTCATCAAGCAACCTTCGATCATCAACATCAAAATAATGTCAACAG 2040
 Db 1981 tcggtcaagcaattcatcagacaccccttcgataccacacaaataatgtcaacag 2040
 Qy 2041 TCTTTAAGCGGATGAAACGCGCTTCTTCTGCGCTTCTGCTGCTGCT 2090
 Db 2041 tctttaacgsgatgaacgsgcgtctctctctctctctctctctctctctctctctctct 2090

RESULT 2

AAF58252/C
 ID AAF58252 standard; DNA; 936 BP.

AC AAF58252;

XX 24-APR-2001 (first entry)

DE Oligonucleotide D1835.

XX Electron-transfer group; ETM; mismatch; genotyping;

KW gene expression; ss.

XX Synthetic.

PN WO200107665-A2.

PD 01-FEB-2001.

PE 26-JUL-2000; 2000WO-US20476.

PR 26-JUL-1999; 9905-0145695.

PR 17-MAR-2000; 2000US-0190259.

XX (CLIN-) CLINICAL MICRO SENSORS INC.

PI Uniek RM;

XX WPI; 2001-159728/16.

XX Nucleic acids containing electron-transfer group, useful as labels in

PT hybridization assays, e.g. for genotyping, allowing repeat analyses on

XX a single surface

CC The present invention relates to a composition comprising two nucleic

AC acids each containing an electron-transfer group (ETM) having

XX different redox potentials. The invention is used for electronic

CC detection of nucleic acids, especially of substitutions (mismatches)

CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.
 XX Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

Query Match 12.7%; Score 266; DB 22; Length 936;
 Best Local Similarly 0.6%; Pred. No. 1.4e-31;
 Matches 5; Conservative 607; Mismatches 172; Indels 0; Gaps 0;

Qy 106 AAAATGGAGATATAGGATTTAGTGAAGAGGCTTTATATATTAAGACTTAATTTGA 165
 Db 787 WWWWWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW
 Qy 166 TTTCAATTTATATATGTAAGAACAGGTATGATGAATTTGATTCATTTATGACTGA 225
 Db 727 WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW
 Qy 226 TGAATAAGTTAACGATTTAGTCTTTTAAATTCATTAATTAATTTTGCCTCAAA 285
 Db 667 WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW
 Qy 286 CTTTGGAAATATATCCATGTTCCGAATTAATTTTGAATAACCAATATCAACCTT 345
 Db 607 WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW
 Qy 346 TTTGCAACAACCTTTTCAAAATTCATTTTCAAGAAAAAATTTACATTAACCTTGC 405
 Db 547 WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW
 Qy 406 AATCAATTTGTATGAATAATTTAAATTTCTTCACTATATATGAACCTCAAGTG 465
 Db 487 WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW
 Qy 466 TTTAAATTTTGAAGAGAGAAAAATGACATTTTCACTTCACTATATATGAACCTCA 525
 Db 427 WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW
 Qy 526 ATGAAATCTTAATTTTATTTAATATATTAATTTCAAGAGCTTAATTTAGAA 585
 Db 367 WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW
 Qy 586 AAGAGAAAAATTAATGACATTTCAATCAAAATCAGATTGTATGATAAATTTAA 645
 Db 307 WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW
 Qy 646 TTTTATTTCAATTTATTTGAACCTCAAGTGTGAACATTTAGAAAAAGAGAAAAATTA 705
 Db 247 WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW
 Qy 706 AATGATGAATAATTTGTAACATCAATTTGTAATGAAATGAAATTTAGAGTGAAG 765
 Db 187 WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW
 Qy 766 AAAAAAAGTGAATTTGTTTATTTGTTTGAATTTTGAATTTTGAATTTTGAATTT 825
 Db 127 WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW
 Qy 826 TGAATTCATCAATAAATATTTATTAATTTACAAAAATGAATTAACAAAAAGAAGA 885
 Db 67 WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW WWWWWW
 Qy 886 AAT 889
 Db 7 WWWWWW 4

RESULT 3

AAF58254/C
 ID AAF58254 standard; DNA; 936 BP.

AC AAF58254;

XX

DT	24-APR-2001 (first entry)
XX	
DE	Oligonucleotide D1875.
XX	
KW	Electron-transfer group; ETW; mismatch; genotyping;
XX	
XX	gene expression; ss.
OS	Synthetic.
XX	
PN	MO200107665-A2.
XX	
PD	01-FEB-2001.
XX	
PF	26-JUL-2000; 2000WO-US20476.
XX	
PR	26-JUL-1999; 99US-0145695.
PR	17-MAR-2000; 2000US-0190259.
XX	
PA	(CLIN-) CLINICAL MICRO SENSORS INC.
XX	
PI	Unex RM;
DR	
XX	
DR	WPI: 2001-159728/16.
XX	
PT	Nucleic acids containing electron-transfer group, useful as labels in
XX	
PT	hybridization assays, e.g. for genotyping, allowing repeat analyses on
XX	
XX	a single surface -
PS	
XX	
XX	Example 6; Page 127; 159pp; English.
XX	
CC	The present invention relates to a composition comprising two nucleic
CC	acids each containing an electron-transfer group (ETW) having
CC	different redox potentials. The invention is used for electronic
CC	detection of nucleic acids, especially of substitutions (mismatches)
CC	and single-nucleotide polymorphisms, e.g. for genotyping,
XX	
XX	monitoring gene expression.
XX	
SO	Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;

	Query Match	Similarity	12.7%	Score 266;	DB 22,	Length 936;
	Best Local	Similarity	0.6%;	Pred. No. 1.4e-31;		
	Matches	5;	Conservative	607;	Mismatches 172;	Indels 0; Gaps 0
Qy	106	AAATGAGATPATAGAAATTAGTTGAAGAAGCGTGTTTATATAATTAGACTTAATTTGA	165			
Db	787	MM	728			
Qy	166	TTCATTTTCATATATCTGAAAACAAGCATGTATGAATTTGGATCATTATGACACTGA	225			
Db	727	MM	668			
Qy	226	TGAAAAAGTTAAGATTAGTTAGTCTTTTTTTTAAATTCCAATATAAATTTTGGCCAA	285			
Db	667	MM	608			
Qy	286	CTTTGCCAAATATTCATGATGTGGGAATATAATTTGAAAAACAACAAATATCAACCTT	345			
Db	607	MM	548			
Qy	346	TTTGCACAACACTTTTACAAAAATCCATTTTCGAAAAAAAATTTACATTAACTTGC	405			
Db	547	MM	488			
Qy	406	AATCAAATTGTGTATGAAAAATTTAAATTTCTTTCACCTATATTTGAACTCAAGTG	465			
Db	487	MM	428			
Qy	466	TTTAAATTTGAAAAGAGAAAAATAAAATGACCATTTCATGCGCAATCAATGTGT	525			
Db	427	MMMTAAGCMNMMMMMMMMMMMMM	368			
Qy	526	ATGAAAAACTTAAATTTTATTTTAAATATATTTGAATTCAAAGICTTAAATTTTGA	565			

[illegible]

XX	AAAF58257/c
XX	AAF58257 standard; DNA; 936 BP.
XX	
AC	AAF58257;
XX	
DT	24-APR-2001 (first entry)
XX	
DE	Oligonucleotide DJ954.
XX	
KM	Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
XX	
OS	Synthetic.
PN	WO200107665-A2.
XX	
PD	01-FEB-2001.
XX	
PF	26-JUL-2000; 2000MO-US20476.
XX	
PR	26-JUL-1999; 99US-0145695.
XX	
PA	17-MAR-2000; 2000US-0190259.
XX	
XX	(CLIN-) CLINICAL MICRO SENSORS INC.
PI	
XX	Umek RM;
DR	
XX	WPT; 2001-159728/16.
XX	
PT	Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface -
XX	
PS	Example 6; Page 127; 159pp; English.
XX	
CC	The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
XX	
SQ	Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other.

Query Match	12.7%;	Score 266;	DB 22;	Length 936;
Best Local Similarity	0.6%;	Pred. No. 1.4e-31;		
Matches	5;	Conservative 607;	Mismatches 172;	Indels 0;
			Gaps	0

QY	106	AAAAAGAGATTAATAGCAATTAGTTGAAAGAGGTGTATATATATAGACTTAATTGA	105
Db	787	AA	728
QY	166	TTCAATTCATATATCTGAAACAAGTATGTAATTTGATTCATTTATGACACTGA	229
Db	727	AA	658
QY	226	TGAAAACGTAAACGATTAGTCTCTTTTAAAAATCCATATAAATTTTGGCCAAA	285
Db	667	AA	608
QY	286	CTTTTCAAAAATATCCATGTTGGAATAAATTTTGAACCAACAATATCAAACTT	345
Db	607	AA	548
QY	346	TTTGGAACCACTTTTACAAAATCCATTTTCAGAAAAAAAATTTACATTAACCTGCA	405
Db	547	AA	488
QY	406	AATCAAAATGTGTGAAAAATTTTAAATTTCTTTGACCTATATATGAACCAAGTG	455
Db	487	AA	428
QY	466	TTTAAATTTAGAAAAAGCAAAAAATAAAAAATGACCATTTTCATGCGAAATCAATTGTG	525
Db	427	AA	368
QY	526	ATGAAAAAATCTAAATTTTATTAATATATATGAATCAAGGTAAATTTAGAA	585
Db	367	AA	308
QY	586	AAGGAAAAAATTTAAATGACCATTTCATTCAAAATCAGATTGTATGAAAAATTTAA	645
Db	307	AA	248
QY	646	TTTTATTTCAAAATATATATGAACCTCAAGTGTGAACATTTTGAAGAGAAAAATTA	705
Db	247	AA	188
QY	706	AAATGATGAAAAATTTGTAACAATCAATTTGTGAATCAGAATTTAGAGTTAGACAAG	765
Db	187	AA	128
QY	766	AAAAAAAACGATTTGTCTAATCTTTGCGTTACAAATTTTGGATCATTAAGAAATTAC	825
Db	127	AA	68
QY	826	TGAATCCATATCAAAAACTATATAATTTACAAAAATGATTAACCAAAAAAACAAGA	885
Db	67	AA	8
QY	886	ACAT 889	
Db	7	AAAA 4	
RESULT 5 AAF58259/c ID AAF58259 standard; DNA; 936 BP.			
XX AAF58259;			
XX 24-APR-2001 (first entry)			
XX Oligonucleotide D2004.			
XX DE Electron-transfer group; ETM; mismatch; genotyping;			

KW gene expression; ss.
 XX Synthetic.
 OS
 XX
 PN WO200107665-A2.
 XX
 PD 01-FEB-2001.
 XX
 PF 26-JUL-2000; 2000WO-US20476.
 XX
 PR 26-JUL-1999; 99US-0145695.
 PR 17-MAR-2000; 2000US-0190259.
 XX
 PA (CLIN-) CLINICAL MICRO SENSORS INC.
 XX
 PI Umek RM;
 XX
 DR WPI; 2001-159728/16.
 XX
 PT Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface -
 XX
 PS Example 6; Page 128; 159pp; English.
 XX
 CC The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETM) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.
 XX
 SO Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;

[illegible]

Db 307 WWWWWW... 248
 QY 646 TTTTATTTCAATATATATGAAACGAGTGAACATTTAGAAAGAGAGAAATTA 705
 Db 247 WWWWWW... 188
 QY 706 AATGATGAATTTGTAAACATCAATTTGTGAATGCAATTTGAAGTTGACACAG 765
 Db 187 WWWWWW... 128
 QY 766 AAAAAAAGTGAATGCTTATCTTGTGATCAATTTGGATCATTAAGCAATTAAC 825
 Db 127 WWWWWW... 68
 QY 826 TGAATTCATATCAAAAACATATATTAATTCAGAAAATGAATTAACCAAAAAAGAGA 885
 Db 67 WWWWWW... 8
 QY 886 ACAT 889
 Db 7 WWW 4

RESULT 6

AAF58262/c
 ID AAF58262 standard; DNA; 936 BP.

AC AAF58262;

DT 24-APR-2001 (first entry)

DE Oligonucleotide D2007.

XX *Electron-transfer group; ETM; mismatch; genotyping;
 KW gene expression; ss.

OS Synthetic.

PN *WO200107665-A2.

PD 01-FEB-2001.

PF 26-JUL-2000; 2000WO-US20476.

PR 26-JUL-1999; 99US-0145695.

PR 17-MAR-2000; 2000US-0190259.

PA (CLIN-) CLINICAL MICRO SENSORS INC.

PI Umek RM;

DR WPI; 2001-159728/16.

XX Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface

PS Example 6; Page 128; 159pp; English.

XX The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETM) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.

XX Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;

Query Match 12.7%; Score 266; DB 22; Length 936;
 Best Local Similarity 0.6%; Pred. No. 1.4e-31;
 Matches 5; Conservative 60%; Mismatches 172; Indels 0; Gaps 0;

QY 106 AAAATGAGATATAGCAATTAGTGAAGAGGTTTATATATAGCAATTAATTTGA 165
 Db 787 WWWWWW... 728
 QY 166 TTCAATTTCAATATCTGAAACAGATGATGAAATTTGATTCATTTATGACTGA 225
 Db 727 WWWWWW... 668
 QY 226 TGAAGAAATTAACGATTTAGTCTTTTAAATTCATATATATTTTGGCCAAA 285
 Db 667 WWWWWW... 608
 QY 286 CTTTGCAAAATATCATGTCGAAATTAATTTGAAAACCAACATATCAACTT 345
 Db 607 WWWWWW... 548
 QY 346 TTTGCAACCACTTTACAAAATCCATTTTCAGAAAAAAATTTACATTAACCTCGA 405
 Db 547 WWWWWW... 488
 QY 406 AATCAATTTGATGAAAAATTTAAATTTCCCTTACCTATATGAACTCAAGTG 465
 Db 487 WWWWWW... 428
 QY 466 TTAATATTTAGAAAGAGAAAAATGAATGACATTTGATGCAATCAATTTGTGT 525
 Db 427 WWWWWW... 368
 QY 526 ATGAAAACTTAATTTTATTTAATATTAATGAATTCAGAGTGTAAATTTGAA 585
 Db 367 WWWWWW... 308
 QY 586 AAGGAAAAATTAATGACCATTTGATGCAATTCATGATGATGATGAAATTTAAA 645
 Db 307 WWWWWW... 248
 QY 646 TTTTATTTCAATATATATGAAACGAGTGAACATTTAGAAAGAGAGAAATTA 705
 Db 247 WWWWWW... 188
 QY 706 AATGATGAATTTGTAAACATCAATTTGTGAATGCAATTTGAAGTTGACACAG 765
 Db 187 WWWWWW... 128
 QY 766 AAAAAAAGTGAATGCTTATCTTGTGATCAATTTGGATCATTAAGCAATTAAC 825
 Db 127 WWWWWW... 68
 QY 826 TGAATTCATATCAAAAACATATATTAATTCAGAAAATGAATTAACCAAAAAAGAGA 885
 Db 67 WWWWWW... 8
 QY 886 ACAT 889
 Db 7 WWW 4

RESULT 7

AAF58255/c
 ID AAF58255 standard; DNA; 938 BP.

AC AAF58255;

DT 24-APR-2001 (first entry)

DE Oligonucleotide D1876.

XX *Electron-transfer group; ETM; mismatch; genotyping;
 KW gene expression; ss.

OS Synthetic.

PN WO200107665-A2.

XX 01-FEB-2001.
 PD
 XX
 PF 26-JUL-2000; 2000WO-US20476.
 XX
 PR 26-JUL-1999; 99US-0145695.
 XX 17-MAR-2000; 2000US-0190259.
 PR
 PA (CLIN-) CLINICAL MICRO SENSORS INC.
 XX
 PI umek RM;
 DR WPI: 2001-159728/16.
 XX
 XX Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface
 XX
 XX Example 6; Page 127; 159pp; English.
 PS
 CC The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETW) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.
 XX
 SQ Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;

Query Match 12.7%; Score 266; DB 22; Length 938;
 Best Local Similarity 0.6%; Pred. No. 1.4e-31;
 Matches 5; Conservative 607; Mismatches 172; Indels 0; Gaps 0;

QY 106 AAAATGGAGTAATAGCAATAGTTGAAAAGGCTTTATTAATTAAGACTTAATTTGA 165
 Db 787 WWWWWW...
 QY 166 TTCAATTCATATCTGAAACAAGTATGTAATGTAATTCATTAATGACTGA 225
 Db 727 WWWWWW...
 QY 226 TGAAGAACTTACAGTTAGTTCTTTTAAATTCATTAATTAATTTTGGCCAAA 285
 Db 667 WWWWWW...
 QY 286 CTTTGCAAAATTCATCTGCGAAATTAATTTGAAAACCAACATATCAACCTT 345
 Db 607 WWWWWW...
 QY 346 TTTCGCAACAATTTTACAAAATCCATTTTCAGAAAAAAAATTTTCATTAATTCGCA 405
 Db 547 WWWWWW...
 QY 406 AATCAATTTGTATGAAAAATTTAAATTTCTTCACCTATTAATTAAGAACTCAAGTG 465
 Db 487 WWWWWW...
 QY 466 TTAATTTTGAAGAGAGAAAAATTAATTAAGCAATTTTCATGCGAAATCAATTTGT 525
 Db 427 WWWWWW...
 QY 526 ATGAAAACTTAATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAAGAA 585
 Db 367 WWWWWW...
 QY 586 AAGGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 645
 Db 307 WWWWWW...
 QY 646 TTTTATTCATATATATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 705
 Db 247 WWWWWW... 188

QY 706 AATGATGAAATTTGTAACATCAATTTGTAATTCAGAAATTTAGAACTGACACAG 765
 Db 187 WWWWWW...
 QY 766 AAAAAACGATGCTTATATCTTTGCTTACATTTTGGGATCATTAAGAAATTAAC 825
 Db 127 WWWWWW...
 QY 826 TGAATCCATATCAAAAATCTATTATAATTAACAAAATGAATAAACCAAAAAAGAGA 885
 Db 67 WWWWWW...
 QY 886 ACAT 889
 Db 7 WWWWWW... 4

RESULT 8

AAF58252
 ID AAF58252 standard; DNA; 936 BP.
 XX
 AC AAF58252;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Oligonucleotide D1835.
 XX
 XX Electron-transfer group; ETW; mismatch; genotyping;
 KW gene expression; ss.
 XX
 OS Synthetic.
 XX
 PN WO200107665-A2.
 PD
 PD 01-FEB-2001.
 XX
 PF 26-JUL-2000; 2000WO-US20476.
 PR
 PR 26-JUL-1999; 99US-0145695.
 PR 17-MAR-2000; 2000US-0190259.
 XX

PA (CLIN-) CLINICAL MICRO SENSORS INC.

PI umek RM;

DR WPI: 2001-159728/16.

PT Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface
 XX

PS Example 6; Page 127; 159pp; English.

CC The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETW) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.
 XX

SQ Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

Query Match 12.7%; Score 264.6; DB 22; Length 936;
 Best Local Similarity 0.8%; Pred. No. 2.3e-31;

Matches 6; Conservative 606; Mismatches 175; Indels 0; Gaps 0;

QY 115 AATATGGAATTAATTTGAAAAGGCTTTATTAATTAATTAATTAATTAATTTGCT 174
 Db 2 WWWWWW... 61
 QY 175 ATATATGCAAAAACAAGTATGTAATTTGATTCATTTATGACACTGATGAAAAAGT 234

```

Db 62 ..... 121
QY 235 TAAAGATTAGTCTTTTAAATTCATATTAATTTTGGCCAAACTTTTGCA 294
Db 122 ..... 181
QY 295 AATATCATGTGGGAATTAATTTGAAAAACAATATCAACCTTTTGGGAC 354
Db 182 ..... 241
QY 355 AACCTTACAAATTCATTTGAGAAAAAATTTACTTACTGCAATCAAT 414
Db 242 ..... 301
QY 415 GTGATGAAAAATTTAAATTTCTTCACCTATTAATGAACTCAAGTTAAATTT 474
Db 302 ..... 361
QY 475 AGAAAGAGAAAAATTAATTAAGACATTTGCAATCAATTTGTATGAAAAAC 534
Db 362 ..... 421
QY 535 TTAAATTTTATTTAATTAATTAATGAAATGTAAGTTAAATTTAGAAAAAGAGAA 594
Db 422 ..... 481
QY 595 AATTAATAAGCATTTTCATTAATCAAGATTTGTATGAAAAATTTAAATTTT 654
Db 482 ..... 541
QY 655 CAATATATTTGAACCAAGTGTGAACATTTAGAAAAAGAGAAAAATTAATTAATGATGA 714
Db 542 ..... 601
QY 715 AAATTTGTAACATTCATTTTGAATTCAGAAATTTAGAAAGTGAAGAAAAAAC 774
Db 602 ..... 661
QY 775 TGAATGTCTTATCTTTGGTGTACATTTTGGGATCATTAAGAAATTTCTGAATCCA 834
Db 662 ..... 721
QY 835 TATCAAAACATTTATTAATTAACAAATGATTAACCAAAAAAGAGACATGACA 894
Db 722 ..... 781
QY 895 TATTTG 901.
Db 782 ..... 788

```

RESULT 9

AAFS8254

ID AAF58254

standard; DNA; 936 BP.

AAF58254;

24-APR-2001 (first entry)

Oligonucleotide D1875.

Electron-transfer group; ETM; mismatch; genotyping;

gene expression; ss.

Synthetic.

W0200107665-A2.

01-FEB-2001.

26-JUL-2000; 2000WO-US20476.

```

PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX Umek RM;
XX WPI: 2001-159728/16.
XX Nucleic acids containing electron-transfer group, useful as labels in
XX hybridization assays, e.g. for genotyping, allowing repeat analyses on
XX a single surface
XX
XX Example 6; Page 127, 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
XX acids each containing an electron-transfer group (ETM) having
XX different redox potentials. The invention is used for electronic
XX detection of nucleic acids, especially of substitutions (mismatches)
XX and single-nucleotide polymorphisms, e.g. for genotyping,
XX monitoring gene expression.
XX
XX Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other:

```

Query Match

12.7%; Score 264.6; DB 22; Length 936;

Best Local Similarity 0.8%; Pred. No. 2.3e-31;

Matches 6; Conservative 606; Mismatches 175; Indels 0; Gaps 0;

```

QY 115 AATATGAGATTTAGTGAAGAGGTTTATATTAATTAAGCTTAATTTGATCATTTTC 174
Db 2 ..... 61
QY 175 ATATATCGAAAAACAAGTATGATGAATTTGATTCATTTATGACACTGATGAAAAAGT 234
Db 62 ..... 121
QY 235 TAAAGATTAGTCTTTTAAATTCATATTAATTTTGGCCAAACTTTTGCA 294
Db 122 ..... 181
QY 295 AATATCATGTGGGAATTAATTTGAAAAACAATATCAACCTTTTGGGAC 354
Db 182 ..... 241
QY 355 AACCTTACAAATTCATTTGAGAAAAAATTTACTTACTGCAATCAAT 414
Db 242 ..... 301
QY 415 GTGATGAAAAATTTAAATTTCTTCACCTATTAATGAACTCAAGTTAAATTT 474
Db 302 ..... 361
QY 475 AGAAAGAGAAAAATTAATTAAGACATTTGCAATCAATTTGTATGAAAAAC 534
Db 362 ..... 421
QY 535 TTAAATTTTATTTAATTAATTAATGAAATGTAAGTTAAATTTAGAAAAAGAGAA 594
Db 422 ..... 481
QY 595 AATTAATAAGCATTTTCATTAATCAAGATTTGTATGAAAAATTTAAATTTT 654
Db 482 ..... 541
QY 655 CAATATATTTGAACCAAGTGTGAACATTTGCAATCAATTTGTATGAAAAAC 714
Db 542 ..... 601
QY 715 AAATTTGTAACATTCATTTTGAATTCAGAAATTTAGAAAGTGAAGAAAAAAC 774
Db 602 ..... 661

```

[illegible]

PI Umek RM;
 XX WPI: 2001-159728/16.
 XX Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface
 XX Example 6; Page 128; 159pp; English.
 PS
 XX The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETM) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.
 XX
 SQ Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;

Query Match 12.7%; Score 264.6; DB 22; Length 936;

Best Local Similarity 0.8%; Pred. No. 2.3e-31;

Matches 6; Conservative 606; Mismatches 175; Indels 0; Gaps 0;

QY 115 ATATAGCAATTGTTGAAAGGTTTATATATAGCTAAATTTGATTCATTTTC 174
 DB 2 WWWWWW
 QY 175 ATATATCTGAAACAGATATGATGAATTTGATTCATTTATGACACTGATGAAAAAGT 234
 DB 62 WWWWWW
 QY 235 TAACGATTAGTCTTTTAAATTCATATATATTTTGGCCAAACTTTTGCA 294
 DB 122 WWWWWW
 QY 295 AATATCATGTTCGAAATTAATTTGAAAAACAATATCAAACTTTTGGGAC 354
 DB -182 WWWWWW
 QY 355 AACTTTTACAAAATTCATTTTCAGAAAAAATTTTACCTTACCTGGCAATCAATTT 414
 DB 242 WWWWWW
 QY 415 GTGATGAAAAATTTAAATTTCTTCACTATATTTGAACCAAGTTTAAATTT 474
 DB 302 WWWWWW
 QY 475 AGAAAGGAGAAAAATTAATGACATTTTCATGCAAAATCAATTTGTATGAAAAAC 534
 DB 362 WWWWWW
 QY 535 TTAATAATTTTAAATATATATGAAATTCAAAGTTTAAATTTAGAAAAAGGAAA 594
 DB 422 WWWWWW
 QY 595 AATTAATATGACATTTTCATCAAAATCAGATGTGTATGAAAAATTTAAATTTTATTT 654
 DB 482 WWWWWW
 QY 655 CAATATATATTTGAAGTCAAGTGAACATTTAGAAAGGAGAAAAATTTAAATGATGA 714
 DB 542 WWWWWW
 QY 715 AAATTTGTAACATTTTGTGAATTCAGAAATTTGAAGTTTACAGAGAAAAAAC 774
 DB 602 WWWWWW
 QY 775 TGAATTTGCTATCTTTTGGTACATTTTGGATCATATTAAGAATTTTCTGAAATCA 834
 DB 662 WWWWWW
 QY 835 TATCAAAAACTATTATATATTAACAAAAATGAATAAACCAAAAAAGAGACATGACGA 894

DB 722 WWWWWW 781
 QY 895 TATTTGCG 901
 DB 782 WWWWWW 788

RESULT 12

ID AAF58262 standard; DNA; 936 BP.

AC AAF58262;

DT 24-APR-2001 (first entry)

DE Oligonucleotide D2007.

KM Electron-transfer group; ETM; mismatch; genotyping;
 KW gene expression; ss.

OS Synthetic.

PN WO200107665-A2.

PD 01-FEB-2001.

PF 26-JUL-2000; 2000WO-US20476.

PR 26-JUL-1999; 99US-0145695.

PR 17-MAR-2000; 2000US-0190259.

PA (CLIN-) CLINICAL MICRO SENSORS INC.

XX Umek RM;

DR WPI: 2001-159728/16.

PT Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface

PS Example 6; Page 128; 159pp; English.

CC The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETM) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.

SQ Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;

Query Match 12.7%; Score 264.6; DB 22; Length 936;

Best Local Similarity 0.8%; Pred. No. 2.3e-31;

Matches 6; Conservative 606; Mismatches 175; Indels 0; Gaps 0;

QY 115 ATATAGCAATTGTTGAAAGGTTTATATATAGCTAAATTTGATTCATTTTC 174
 DB 2 WWWWWW
 QY 175 ATATATCTGAAACAGATATGATGAATTTGATTCATTTATGACACTGATGAAAAAGT 234
 DB 62 WWWWWW
 QY 235 TAACGATTAGTCTTTTAAATTCATATATTTTGGCCAAACTTTTGCA 294
 DB 122 WWWWWW
 QY 295 AATATCATGTTCGAAATTAATTTGAAAAACAATATCAAACTTTTGGGAC 354
 DB 182 WWWWWW

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QY 355 AACTTTACAAAATCCATTTTCAGAAAAAAATTTACATTACTGGCAATCAATT 414
Db 242 .....
QY 415 GTGTATGAAAAATTTAAATTCCTTCACCTATATGAACTCAAGTGTAAATTT 474
Db 302 .....
QY 475 AGAAAAAGGAAAAATTTAAATTTGACCATTTTCGCAATCAATTGTGTGAAAAC 534
Db 362 .....
QY 535 TTAATATTTTATTTAAATATATGAAATTCAGAGTGTAAATTTGAAAAAGGAAA 594
Db 422 .....
QY 595 AATTAAATGACCATTTTCATTCAAAATGAGATTGTATGAAAAATTTAAATTTTATTT 654
Db 482 .....
QY 655 CAATATATATGAACTCAAGTGTGAACATTTAGAAAAAGGAAAAATTTAAATGATGA 714
Db 542 .....
QY 715 AATTTGTAAACATCAATTTGTGAAATCAGAAATTTAGCAAGTTAGACAAGAAAAAAC 774
Db 602 .....
QY 775 TGAATGCTTATCTTTTCGGTTACAAATTTGGGATCATAAGAAATTTACTGAATCCA 834
Db 662 .....
QY 835 TATCAAAACATATTTAAATTTACAAAATTTGATTTAAACCAAAAAAGAGACATGACGA 894
Db 722 .....
QY 895 TATTTGCG 901
Db 782 .....

```

RESULT 13

AAFS8255

ID AAF58255 standard; DNA; 938 BP.

AC AAF58255;

DT 24-APR-2001 (first entry)

DE Oligonucleotide D1876.

KM Electron-transfer group; ETM; mismatch; genotyping;

OS Synthetic.

PN WO200107665-A2.

PD 01-FEB-2001.

PE 26-JUL-2000; 2000MO-US20476.

PR 26-JUL-1999; 99US-0145695.

PR 17-MAR-2000; 2000US-0190259.

PA (CLIN-) CLINICAL MICRO SENSORS INC.

PI Umek RM;

DR WPI; 2001-159728/16.

PT Nucleic acids containing electron-transfer group, useful as labels in

```

PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
PS Example 6; Page 127; 159pp; English.
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;

Query Match 12.7%; Score 264.6; DB 22; Length 938;
Best Local Similarity 0.8%; Pred. No. 2,3e-31;
Matches 6; Conservative 606; Mismatches 175; Indels 0; Gaps 0;

QY 115 ATATATGCAATTTAGTGAAGAGGTGTATATATATGACTTAAATTTGATTCATTTTC 174
Db 2 .....
QY 175 ATATATGCAAAACAGTATGTATGAAATTTATTCATTTATGACACTGATGAAAAAGT 234
Db 62 .....
QY 235 TAACGATTTAGTCTTTTAAATTTCCATATATATTTTGGCCAAACCTTTTGCAA 294
Db 122 .....
QY 295 AATATCCATTTGGAATTAATTTGAAAAACAAATATCAACCTTTTGGCAAC 354
Db 182 .....
QY 355 AACTTTACAAAATCCATTTTCAGAAAAAAATTTTACATTACTGGCAATCAATTT 414
Db 242 .....
QY 415 GTGTATGAAAAATTTAAATTCCTTCACCTATATGAACTCAAGTGTAAATTT 474
Db 302 .....
QY 475 AGAAAAAGGAAAAATTTAAATTTGACCATTTTCGCAATCAAAATTTGTATGAAAAAC 534
Db 362 .....
QY 535 TTAATATTTTATTTAAATATATGAAATTCAGAGTGTAAATTTGAAAAAGGAAA 594
Db 422 .....
QY 595 AATTAAATGACCATTTTCATTCAAAATGAGATTGTATGAAAAATTTAAATTTTATTT 654
Db 482 .....
QY 655 CAATATATATGAACTCAAGTGTGAACATTTAGAAAAAGGAAAAATTTAAATGATGA 714
Db 542 .....
QY 715 AATTTGTAAACATCAATTTGTGAAATTCAGAAATTTAGCAAGTTAGACAAGAAAAAAC 774
Db 602 .....
QY 775 TGAATGCTTATCTTTTCGGTTACAAATTTGGGATCATAAGAAATTTACTGAATCCA 834
Db 662 .....
QY 835 TATCAAAACATATTTAAATTTACAAAATTTGATTTAAACCAAAAAAGAGACATGACGA 894
Db 722 .....
QY 895 TATTTGCG 901

```

Db 782 www.wmg 788

RESULT 14

AA33181
ID AAX33181 standard; DNA: 6644 BP.

XX AAX33181;

XX 25-JUN-1999 (first entry)

XX Base sequence of the plasmid pKx-lres-bsr.

XX Cowpox virus; bsr; viral vector; expression; apoptosis; resistance;
XX crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer;
XX autoimmune disease; graft rejection reaction; inflammation;
XX inflammatory disease; ss.

OS Synthetic.

OS Cowpox virus.

XX W09913073-A2.

XX 18-MAR-1999.

XX 07-SEP-1998; 98WO-JP04010.

XX 08-SEP-1997; 97JP-0259235.

XX (RPRG-) RPR GENCELL ASIA PACIFIC INC.

XX Hamada H;

XX WPI: 1999-243728/20.

XX New apoptosis-resistant virus-sensitive cell

XX Example 1; Page 38-41; 51pp; English.

XX The present invention describes an apoptosis-resistant virus-sensitive
 CC cell line into which an apoptosis resistance gene has been introduced.
 CC The recombinant viruses generated are capable of expressing apoptosis-
 CC associated genes. These can then be used in a variety of diseases for
 CC which the induction of apoptosis by gene transfer, or where the
 CC inhibition of harmful apoptosis, is therapeutic. The recombinant viruses
 CC are useful as vectors for gene therapy which can be applied to cancer
 CC therapy for destroying cancer cells selectively, the treatment of
 CC autoimmune diseases and graft rejection reaction, and apoptosis induction
 CC therapy for inflammatory cells in inflammatory diseases. Prior arts have
 CC encountered the problem where if an adenovirus vector capable of
 CC expressing an apoptosis-associated gene is introduced into animal cells,
 CC the cells producing the virus will be destroyed because the period of
 CC time required to induce cell death by apoptosis is shorter than that
 CC required to replicate and produce the virus, resulting in failure to
 CC obtain a recombinant virus having the integrated apoptosis-associated
 CC gene. In this invention an apoptosis-resistant 293 line (having an
 CC apoptosis resistant gene introduced) is established and overcomes the
 CC problem. The present sequence represents the base sequence of the
 CC plasmid pKx-lres-bsr, which contains the cowpox virus bsr gene, and
 CC is used in an example from the present invention.

Sequence 6644 BP; 2166 A; 1573 C; 1424 G; 1481 T; 0 other;

Query Match 6.3%; Score 131; DB 20; Length 6644;

Best Local Similarity 49.3%; Pred. No. 1.6e-11;
Matches 341; Conservative 0; Mismatches 350; Indels 0; Gaps 0;

QY 322 AAAAAAACAATCAATCACTTTGGACACACTTTACAAAATCAATTTACAGAA 381
 Db 3741 aa 3800
 QY 382 AAAAAAATTTACATTAAGTGAATCAATGTTGTATGAAAAATTTAAATTCCTT 441

Db 3801 aa 3660
 QY 442 CACCTATATTTGAAGTCAAGTGTAAATTTAGAAAAAGGAAAAATTAATAATGACC 501
 Db 3861 aa 3920

QY 502 ATTTCATGCGAATCAATTTGTGTATGAAAAACTTAAATTTTATTTAAATATATGA 561
 Db 3921 aa 3980

QY 562 AATTCAAGTGTAAATTTAGAAAAAGCAAAAAATTAATGACCATTTCAATCAAAAT 621
 Db 3981 aa 4040

QY 622 CAGATTGTATGAAAAATTTAAATTTTATTTCAATATTAATTTCAAACTGGA 681
 Db 4041 aa 4100

QY 682 ACATTTGAAAGAGAAAAATTAATGATGAATTTGTAAACATCAATTTGTGAA 741
 Db 4101 aa 4160

QY 742 TCAGATTTAGAGTTAGACAGAAAAAAACCTGAATTTCTTATPACTTTTGGTTACA 801
 Db 4161 aa 4220

QY 802 ATTTTGGATCATTAAGAAATTTACTGAATCCATATCAAAAATTTAAATTCACAAA 861
 Db 4221 aa 4280

QY 862 ATGATTAATAACCAAAAAAGACACATGACATATTTGTAAGACATCACTACTGATT 921
 Db 4281 aa 4340

QY 922 ATAAAGACATGCGCATTTAGATTGAGAACAAAACTTTCAAAATTCACAAAAT 981
 Db 4341 aa 4400

QY 982 GGATNACAACTACCAAGAACATGAAAGAT 1012
 Db 4401 aaaaaaaaaaaaaaaaaaaaaaaaaaagaact 4431

RESULT 15

AA33182
ID AAX33182 standard; DNA: 7372 BP.

XX AAX33182;

XX 25-JUN-1999 (first entry)

XX Base sequence of the plasmid pKx-bcl-x1-bsr.

XX Cowpox virus; bsr; viral vector; expression; apoptosis; resistance;
 XX crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer;
 XX autoimmune disease; graft rejection reaction; inflammation;
 XX inflammatory disease; ss.

OS Synthetic.

OS Homo sapiens.

XX W09913073-A2.

XX 18-MAR-1999.

XX 07-SEP-1998; 98WO-JP04010.

XX 08-SEP-1997; 97JP-0259235.

XX (RPRG-) RPR GENCELL ASIA PACIFIC INC.

XX Hamada H;

Sat Feb 23 11:04:38 2002

us-09-636-826-1.rng

Page 14

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2002, 05:19:02 ; Search time 53.82 Seconds
(without alignments)
8794.854 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 351203 seqs, 11328999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	4.6	19124	2 US-08-487-826B-13	Sequence 13, Appl
2	75.2	3.6	615	4 US-08-998-416-186	Sequence 186, App
3	74	3.5	5852	1 US-07-867-106-2	Sequence 2, Appl
4	73.6	3.5	837	4 US-08-998-416-288	Sequence 288, App
5	72.6	3.5	665	2 US-08-883-795A-36	Sequence 36, Appl
6	70.8	3.4	658	4 US-08-998-416-595	Sequence 595, App
7	69.4	3.3	7218	1 US-08-232-463-14	Sequence 14, Appl
8	69.4	3.3	19124	2 US-08-487-826B-13	Sequence 13, Appl
9	69.2	3.3	636	4 US-08-998-416-1137	Sequence 1137, Ap
10	68.6	3.3	8920	2 US-09-056-075-1	Sequence 1, Appl
11	68.4	3.3	8920	4 US-09-150-741-1	Sequence 1, Appl
12	68.4	3.3	8920	4 US-07-991-867B-41	Sequence 41, Appl
13	66	3.2	1689	1 US-08-544-332-41	Sequence 41, Appl
14	66	3.2	3095	6 5231168-1	Patent No. 5231168
15	66	3.2	8457	1 US-07-991-867B-1	Sequence 1, Appl
16	66	3.2	8457	2 US-08-544-332-1	Sequence 1, Appl
17	66	3.2	8457	2 US-08-517-926-27	Sequence 27, Appl
18	65.6	3.1	4818	1 US-07-991-867B-8	Sequence 8, Appl
19	65	3.1	1511	1 US-08-107-755A-8	Sequence 8, Appl
20	65	3.1	1511	2 US-08-544-332-8	Sequence 8, Appl
21	65	3.1	2447	2 US-09-014-969-14	Sequence 14, Appl
22	65	3.1	51952	2 US-08-947-823-1	Sequence 1, Appl
23	64.8	3.1	3933	2 US-08-731-722-3	Sequence 3, Appl
24	64.6	3.1	3933	2 US-08-731-722-3	Sequence 3, Appl
25	64.6	3.1	3933	2 US-08-731-722-3	Sequence 3, Appl
26	64.4	3.1	51952	2 US-08-947-823-1	Sequence 1, Appl
27	63.6	3.0	2539	3 US-08-749-522-3	Sequence 3, Appl

28	63.4	3.0	1431	4 US-09-316-083-2	Sequence 2, Appl
29	63.2	3.0	1511	1 US-07-991-867B-8	Sequence 8, Appl
30	63.2	3.0	1511	1 US-08-107-755A-8	Sequence 8, Appl
31	63.2	3.0	1511	2 US-08-544-332-8	Sequence 8, Appl
32	62.4	3.0	7218	1 US-08-232-463-14	Sequence 14, Appl
33	62.2	3.0	240	1 US-08-628-417-6	Sequence 6, Appl
34	61.6	2.9	2030	2 US-08-705-937-7	Sequence 7, Appl
35	60.8	2.9	6243	2 US-09-056-075-1	Sequence 1, Appl
36	60.6	2.9	827	4 US-08-998-416-535	Sequence 535, App
37	60.4	2.9	665	2 US-08-883-795A-36	Sequence 36, Appl
38	60.4	2.9	782	4 US-09-007-119-15	Sequence 15, Appl
39	60.2	2.9	732	4 US-08-998-416-1036	Sequence 1036, Ap
40	60.2	2.9	4140	3 US-08-894-731-2	Sequence 2, Appl
41	59.8	2.9	6152	4 US-08-973-462-1	Sequence 1, Appl
42	59.6	2.9	1676	4 US-09-009-443-1	Sequence 10, Appl
43	59.4	2.8	5181	1 US-08-257-073-10	Sequence 1, Appl
44	59.4	2.8	6768	1 US-08-107-755A-1	Sequence 1, Appl
45	59	2.8	1230	4 US-09-140-466-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-487-826B-13
Sequence 13, Application US/08487826B
Patent No. 593827

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Israelson, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NH121.001CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-826B-13

Query Match

4.6%; Score 97; DB 2; Length 19124;

Best Local Similarity 49.6%; Pred. No. 3e-09;
Matches 304; Conservative 0; Mismatches 305; Indels 4; Gaps 2.

[illegible]

RESULT 2
Sequence 186, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippssen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jürgen
APPLICANT: Knechtle, Philipp
APPLICANT: Reibschunig, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBAYA GOSSTYPI
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.330
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weis, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAGO74RP

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Query Match	3.68;	Score 75.2;	DB 4;	Length 615;
Best Local Similarity	46.1%;	Pred. No. 1.5e-05;		
Matches 251, conservative	0;	Mismatches 293;	Indels 0;	Gaps 0

QY	319	TTGAAAAACAAAACAAATTCACAAACCTTTGGCAGACACCTTTTACAAAATCCATTTTCA	378
Db	587	TTAAATTAAGATTAATATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	528
QY	379	GAATAAAAAATTTACATTACCTGCGAATCAAAATGGTAGAAAAATTTAAATTTCC	438
Db	527	ATGAAATATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	468
QY	439	TTTCACCTTAATTTGAAACTCAAGTGTTAAATTTAGAAAAGGAAAAATTAATAATG	498
Db	467	TTTTAATTAATTAATCTTTAAAGGTAAATTAATTAATTAATTAATTAATTAATTA	408
QY	499	ACCATTCATGCGAATCAAAATTTGATGCGAAAACCTTAAATTTATTTTAATATAT	558
Db	407	TGATGTTTATTAATTAATAATTAATTTTCATATTTTAATTAATTAATTAATTAATTA	348
QY	559	TGAATTTCAAGTGTAAATTTAGAAAAGGAGAAAAATTAATTAATGACATTCATCA	618
Db	347	TAAATATATTTATTTAATTAACAAATTAATTAATTAATTAATTAATTAATTAATTA	288
QY	619	AATCAGATGTGTATGAAAAATTTTAATTTTATTTCAAATATATTAATGAAATCGAAATG	678
Db	287	TAAATATTTATTAAGAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	228
QY	679	TGAACATTTAGAAAAGGAAAAATTTAAATGATGAAAAATTTGTAACATCAATTTGTG	738
Db	227	TGAACATGAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	168
QY	739	AAATCAGAAATTTAGAGTTAGCAAGAAAAAAAACGAATTCCTATACCTTTTGGTT	798
Db	167	TAAATGATGATTAAGTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTA	108
QY	799	ACAAATTTGGGATCATTAAGAAATTAAGTAATTCATTAATTAATTAATTAATTAAT	858
Db	107	TAAATTTAAATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	48
QY	859	AAAA 862	
Db	47	AAAA 44	

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QY 510 CGAATTCGAATTTGGTATGGAAGAAACCTTAAATTTTATTTAAATATATGAAATTCGAA 566
Db 2132 ATAAATTTAAATTTGCATGCGCCAAAAGCTATATATTTGGATATATATATCCAAATATTTATTA 2133
QY 570 GTGTTAAATTTAGAAAAAGGAGAAAAATTTAAATGACCATTTCTTCATAAATCAGATTTGT 629
Db 2132 ATAAAGTATATTTAGATAGAGAAATTAATTTTAAATTTTAAATTTTAAATAAAAAAATCAAAAAA 2073
QY 630 GTATGAAAAAATTTAAATTTTATTTTCAAAATATATTGAAACCTCAAAAGTGAACATTTAG 689
Db 2072 ACCAAAGTAATTAATTAATTTAATGAGGGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTT 2013
QY 690 AAAAGAGCAAAATTAATTAATGATGAAAAATTTGTAAACAATTCATTTTGTCAATTCGAAAT 749
Db 2012 CAAAGTAAAAAATAAAAAAAAAAAAAAAAAAGAAATGAAAAAAGTTGGTTAACTATCAATTT 1953
QY 750 TAGAAGTTAGA-----CAAGGAAAAAATAACGATATGCTTATTTACTTTTTCGGTTCAAT 804
Db 1952 AGTTTTTATTTAGTTTGTTCATATTTTAAATAATCACTTTTATTTTAAATTTGATTTTAAAT 1893
QY 805 TTGGATCATTAAGAAATTTACTGAATTCATATCAAAAACTTTATTAATTTCAAAAAATG 864
Db 1892 ATGAGACTATATTAATAAAAAAAAAAATTTTAAATTTTAAATAAAAAAGAAAAAATAAAAAA 18333
QY 865 AATTAACCAAAAAAAGACAGACATCGCATTTTGTGTAAGACATCATCTACTGATTTA 924
Db 1832 AGTAGAATTTATTTAAATAATTTAAATATTTATTTCAATCTTTATTAATAATTAAGTATATATGAT 1773
QY 925 AAGACATCGGCATATTTAGAAATTTGAGAAACAA 958
Db 1772 AGGCAATTTATTTTATATCTATCTATAAAAAA 1739

RESULT 4
US-08-998-416-288/c
; Sequence 288, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Corinne
; APPLICANT: Redischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSTYPI
; TITLE OF INVENTION: AND USUS THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/998,416
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 919-541-8587
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 288:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 837 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: PAG1241RP
 US-08-998-416-288

Query Match 3.5%; Score 73.6; DB 4; Length 837;
 Best Local Similarity 47.8%; Pred. No. 3e-05;
 Matches 282; Conservative 0; Mismatches 299; Indels 9; Gaps 2;

162 TTGATTCATTTTCATATATCTGAAACAGGATGATGAAATTTGATTCATTTATGACA 221
 11
 Db 597 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 538
 11
 Qy 222 CTGATGAAAGGTTAAGCATTTAGTCTTTTAAATTCATATTAATTTTCC 281
 11
 Db 537 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 478
 11
 Qy 282 AAAACCTTTGCAAAATATCATGTTGCGAAATTAATTTGAAAAACAAATATCAAA 341
 11
 Db 477 TAAATTAATTTTAAATTAATTAATTCCTTAATAAAGATTAAATTAATCAACATATA 418
 11
 Qy 342 CCTTTTGCAGAACCTTTTCCAAAATCCATTTTCAGAAAAAAAATTTTCATTAATCT- 400
 11
 Db 417 TTTATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATC 358
 11
 Qy 401 -----TGCGAATCAATTTGTATGAAAAATTTAAATTTCCCTTACCTTAATG 453
 11
 Db 357 TTTATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATG 298
 11
 Qy 454 AAACCTCAAGTGTAAATTTTGAAGAGAGAAAAATTAATAAGACATTTTCGCGAA 513
 11
 Db 297 AATAATCTATTAAATTAATTAATTAATTAAGAAAAATTAATTAATTAATTAATTAATTA 238
 11
 Qy 514 ATCAATATGTTGATGAAAACTTAAATTTTAAATTTTAAATTTGAAATTCGAAATG 573
 11
 Db 237 ATTTAAATTTGACATGACATTAATTAATTAATTAATTAATTAATTAATTAATTA 178
 11
 Qy 574 TAAATTTAGAAAGAGAGA-AAATTAATTAATGACATTTTCATTCAAATTCGATTTG 632
 11
 Db 177 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 118
 11
 Qy 633 TGAATAATTTAAATTTTATTTCAATTAATTAATTAATTAATTAATTAATTAATTA 692
 11
 Db 117 ATCAATTAATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 58
 11
 Qy 693 AGCAGAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 742
 11
 Db 57 ATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8

RESULT 5
 US-08-883-795A-36
 Sequence 36, Application US/08883795A
 Patent No. 5985607

GENERAL INFORMATION:
 APPLICANT: Delcive, Genevieve
 APPLICANT: Awang, Gregor
 TITLE OF INVENTION: Recombinant DNA Molecules and Expression
 TITLE OF INVENTION: Vectors for Tissue Plasmidogen Activator
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERESKIN & PARR
 STREET: 40 King Street West
 CITY: Toronto

STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/883,795A
 FILING DATE: 27-JUN-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Gravelle, Micheline
 REGISTRATION NUMBER: 40,261
 REFERENCE/DOCKET NUMBER: 7841-062
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 665 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: Rh 32
 US-08-883-795A-36

Query Match 3.5%; Score 72.6; DB 2; Length 665;
 Best Local Similarity 48.4%; Pred. No. 4.4e-05;
 Matches 290; Conservative 0; Mismatches 304; Indels 5; Gaps 3;

411 AATTGTGTATGAAATTTAAATTTCTTTGACATTAATTAATTAATTAATTAATTAATTA 470
 11
 Db 14 AATTGTGTATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 73
 11
 Qy 471 ATTAGAAAGAGAAAAATTAATAATGACATTTTCATGCGAAATCAATTTGTATGAA 530
 11
 Db 74 ATT-AAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 131
 11
 Qy 531 AAACCTTAATTTTATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 590
 11
 Db 132 TAAATTAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 191
 11
 Qy 591 GAAAAATTAATTAATGACATTTTCATTCAAATTCAGATTTGTATGAAAAATTTT 650
 11
 Db 192 TAAATTAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 251
 11
 Qy 651 ATTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 708
 11
 Db 252 TAAATTAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 311
 11
 Qy 709 TGATGAATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 768
 11
 Db 312 TAAATTAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 371
 11
 Qy 769 AAAAATGAATTTCTTATTAATTTTGGTTACAAATTTGGGATTCATTAAGAAATTA 828
 11
 Db 372 TAAATTAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 431
 11
 Qy 829 AATCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 887
 11
 Db 432 TAAATTAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 491
 11
 Qy 888 ATGAGATTTTGTGAAGAACATCAATGATTAATTAATTAATTAATTAATTAATTAATTA 947
 11
 Db 492 TAAATTAATTTATTAATTAATTAATTTTATTAATTAATTAATTAATTAATTAATTA 551

QY 948 TGAGAAACAAAACCTATTTCACAAAATGAGATACACATACAGAACATGA 1006
 DB 552 TCAATATTTTATTAATAGTTAAAGACGAGAGAAAATTAAGAGAGAGTTATTCGA 610

RESULT 6

US-08-998-416-595/c

; Sequence 595, Application US/08998416
 ; Patent No. 6239264

GENERAL INFORMATION:

APPLICANT: Philippson, Peter
 APPLICANT: Pohlmann, Rainer
 APPLICANT: Steiner, Sabine
 APPLICANT: Mohr, Christine
 APPLICANT: Wendland, Jürgen
 APPLICANT: Knechtle, Philipp
 APPLICANT: Redischung, Corinne
 TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSEYII
 TITLE OF INVENTION: AND USES THEREOF
 NUMBER OF SEQUENCES: 1152
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 6239264artis Corporation
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: No. 6239264th Carolina
 COUNTRY: USA
 ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/998.416
 FILING DATE: 24-DEC-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: CH 0016/97
 FILING DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8587
 TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 595:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 658 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: PAG1408RP

US-08-998-416-595

Query Match

Best Local Similarity 3.48; Score 70.8; DB 4; Length 658;
 Pred. No. 9.2e-05;

Matches 236; Conservative 0; Mismatches 257; Indels 1; Gaps 1;

QY 477 AAAAGGAGAAATATAAATGACCATTTATGCGAAATCAAAATGTGTATGAAAACTT 536
 DB 653 AAAATATAATTAATATAATATAATATAATATAATATAATATAATATAATATA 594
 QY 537 AAA-ATTTATTTAATATATATGAATCAAGTCTAAATTTAAGAAAGAGAGAAA 595
 DB 593 AAATATAATATAATATAATATAATATAATATAATATAATATAATATAATATA 534
 QY 596 ATTAATATGACATTTCAATCAAAATCAGATTTGTATGAAAAATTTAATTTTATTC 655
 DB 533 AGAAATAGCATATATATATATGTCACAAATCAATCTATATATGAATTAAGTACCAAT 474

QY 656 AATATATATGAACCTCAAGCTGTGACATTTGACAAAAGAGAGAAAAATTAATGATGAA 715
 DB 473 AATATACTATCTAT 414
 QY 716 AATTTGTAAGACATCAATTTGTGAATCAGATTTTGAAGTTGACAGAGAAAAAACT 775
 DB 413 AAATATACTAATATAAAGAGTAAATATAAATAAATAAATAAATAAATAAATAA 354
 QY 776 GAATTTGCTATACCTTTTCGTTACATTTTGGGATCATTAAGAAATTCGAAATTCAT 835
 DB 353 AAATATAATATAATATAATATAATATAATATAATATAATATAATATAATATAAT 294
 QY 836 ATCAAAACATTTATATAATTCACAAAATGATTAACCAAAAAAGAGAGACATGACAT 895
 DB 293 AATATAATATAATATAATATAATATAATATAATATAATATAATATAATATAAT 234
 QY 896 ATTTCTGAAGACATCATCTGATTTATAAAGACATGCGCATTTAGATGAGAAAC 955
 DB 233 AATATAATATAATATAAATAATATAATATAATATAATATAATATAATATAATATA 174
 QY 956 AAAAATCTATTCOA 969
 DB 173 CAAAGCATCTMAAA 160

RESULT 7

US-08-232-463-14/c

; Sequence 14, Application US/08232463
 ; Patent No. 5670367

GENERAL INFORMATION:

APPLICANT: DORNER, F.
 APPLICANT: SCHEIFLINGER, F.
 APPLICANT: FALKNER, F. G.
 TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-0299

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,463
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/935,313
 FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6
 FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 30472/114 IMMU
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)836-9300
 TELEFAX: (703)683-4109

INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

MOLECULE TYPE: linear
 IMMEDIATE SOURCE:
 CLONE: pTZ9pt-F15

US-08-232-463-14

Query Match	3.3%;	Score 69.4;	DB 1;	Length 7218;
Best Local Similarity	8.4%;	Pred. No. 0.00021;		
Matches 37;	Conservative 230;	Mismatches 176;	Indels 0;	Gaps 0;

Oy	569	AGTGTAAATTTTGGAAAGGAGAAAAATTTAAATGACCATTCATTCGAAATCGAGTTG	628
Dd	1513	AGTTTCAAAAACGGCATTGAGSCATCAGCTGTAATTACTACTCTATGCAAGTACTAAAG	1454
Oy	629	TGTATGAAAATTTAAATTTTATTTCCTAAATATATGAAACTCAAAGTGGACATTTA	688
Dd	1453	AGATAGAGAAGATTTGTGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	1394
Oy	689	GAAAGGAGAAAATTTTAAATGATGAAAATTTTAAACATCAATTTGGAAATCAGAT	748
Dd	1393	RR	1334
Oy	749	TTAGAGTTAGACAAGAAAAAAACTGAATTTGCTTATACTTTGGTTACATTTTGG	808
Dd	1333	RR	1274
Oy	809	GATCATTAAGAAATTTACTGGAATTCATATCAAAAACATATTATTAATACAAAAAGATA	868
Dd	1273	RR	1214
Oy	869	AAACCAAAAAAGAGAACATGACGATTTCTTAAGAACATCAGATGATTATAAAG	928
Dd	1213	RR	1154
Oy	929	AACATGGCATATTAGATTTGAGAAACAAAAAACTATTCAAATTCAAAAATGCATAAC	988
Dd	1153	RR	1094
Oy	989	AACATCAAAAACATGAAAAG	1011
Dd	1093	RRRRRRRRRRRRRRRRRRRRRR	1071

RESULT 8
 US-08-487-826B-13/c
 ; Sequence 13, Application US/08487826B
 ; Patent No. 5993827
 ;
 GENERAL INFORMATION:
 ;
 APPLICANT: Sim, Kim L.
 APPLICANT: Chitnis, Chetan
 APPLICANT: Miller, Louis H.
 APPLICANT: Peterson, David S.
 APPLICANT: Su, Xin-zhaun
 APPLICANT: Wellens, Thomas E.
 TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
 ;
 NUMBER OF SEQUENCES: 45
 ;
 TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
 ;
 CORRESPONDENCE ADDRESS:
 ;
 ADDRESSEE: Knobbe Martens Olson & Bear
 ;
 STREET: 620 Newport Center Drive 16th Floor
 ;
 CITY: Newport Beach
 ;
 STATE: California
 ;
 COUNTRY: US
 ;
 ZIP: 92660
 ;
 COMPUTER READABLE FORM:
 ;
 MEDIUM TYPE: Floppy disk
 ;
 COMPUTER: IBM PC compatible
 ;
 OPERATING SYSTEM: PC-DOS/MS-DOS
 ;
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 ;
 CURRENT APPLICATION DATA:
 ;
 APPLICATION NUMBER: US/08/487,826B
 ;
 FILING DATE: 10-SEP-1993
 ;
 CLASSIFICATION: 435
 ;
 ATTORNEY/AGENT INFORMATION:
 ;
 NAME: Israelsen, Ned
 ;
 REGISTRATION NUMBER: 29,655
 ;

```

1 REFERENCE/DOCKET NUMBER: NIN121.001CPI
2 TELECOMMUNICATION INFORMATION:
3 TELEPHONE: (619) 235-8550
4 TELEFAX: (619) 235-0176
5 INFORMATION FOR SEQ ID NO: 13:
6
7 SEQUENCE CHARACTERISTICS:
8
9 LENGTH: 19124 base pairs
10
11 TYPE: nucleic acid
12
13 STRANDEDNESS: single
14
15 TOPOLOGY: linear
16
17 MOLECULE TYPE: cDNA
18
19 HYPOTHEetical: NO
20
21 ANTI-SENSE: NO
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Query Match	3.38;	Score 69.4;	DB 2;	Length 19124;
Best Local Similarity	46.18;	Pred. No. 0.00023;		
Matches 350;	Conservative	0;	Mismatches 396;	Indels 13;
				Gaps 3

QY	54	TTTTTAACTCTCAAACTTTTTCACACTTTAGTGACATTAATGTAGTTGAAAAATGGA	113
Db	18352	TTTTTTTTTTTTTTTTTTTTTTTGTGATATGTAGTAATTACTTATAGTTTTTGTGGAT	18293
QY	114	GATAATAGCAATTAAGTAAAAAGGGTGTTATATATATAGACTTAATTCATTCATTTT	173
Db	18292	AAAACAATTAGCAATTAATAAAGCAATTAAGCTTAATTAATAATTAAGAAATAGTTATAT	18233
QY	174	CATATATCGAAGAACAGGTATGTATGAATTTGATTCATTTATGACCTGATGAAAAAG	233
Db	18232	TATAAAAATTAACAAATAATATTATGTATATATATATATATTTATTTATATAGCAACTAT	18173
QY	234	TTAAGCAT-----TTAGTCTCTTTTAAAAATTCCAATTAATTTTTCGCCAAACT	287
Db	18172	ATTAATATTTGATTAATTAATATTTTTTTATATGAGATTATATATTTTTTTTGGCTGGATT	18113
QY	288	TTTGGCAAAATATCCATGTTGGCAATTAATTTTGGAAAAACAACATATCAACTTTT	347
Db	18112	ATTCAGAATTTAGATAACAAATAATTAACACACTATATTAACACATATTAATACACAT	18053
QY	348	TGCGAACAACTTTACAAAAATCCATTTTCAGAAAAAAAATTTTCATT-----AAGCT	401
Db	18052	TTTAATTAATATTTTATAAAATTCACAAATTAATTAATTAATTAATTAATTAATCTGCAAAAAATATG	17993
QY	402	GGCAATCCAAATTTGTATGAAAAATTTTAAATTTCCCTTCCACTCAATTAATGAAACTGA	461
Db	17992	AAAAATCGAAATAGAGGATATATATTTTGAAAAAGAGATTTATATATATATATATA	17933
QY	462	AGTGTAAATTTAGAAAAAGAAAAATTAATAATGACACTTTCATGCGGAATCAATTT	521
Db	17932	TTATATATATACGAAAAAATGTACAGAAAAAACAACCAATTAACCATATATATACATAATT	17873
QY	522	GTGTATGAAAACTTAAATTTTATTTTAAATATATATTAATTTGAATTTCAAGTGTTAAATTT	581
Db	17872	ATTAAATCAAAATAGATGACAAATTAATTTATCTAAAAAATTAATTAATATATATATATAA	17813
QY	582	AGAAAGGAGAAATTAATTAATGACCATTTCAATTCAAATTCAGATTTGTGTGATGAAAAATT	641
Db	17812	TATTTATGAAAAAATTTACCAATTAAGAAAAAATAAATTAATCATGTCTGCCAATTTATTA	17753
QY	642	TAAATTTTATTTCAATTAATTAATGAACTCAAGTGTGACATTTAGAAAAAGGAAAA	701
Db	17752	AAATATATATATATATGATTTTAAACAACAAACATATTTTTTACAAATATACAAAAACAATA	17693
QY	702	ATTAAATGATGAAAAATTTGTAAACATCAATTTTGGA--ATCAGATTTTAAAGTTAGA	760
Db	17692	AAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATGACA	17633
QY	761	CAAGGAAAAAAACGATTTGCTGTTTACTTTTCGCTTA	799
Db	17632	CAACGAAAAAAGTATATTTAATTTTATGATATTTCCATATA	17594

[illegible]

Qy	606	CCATTTCATTCGAAAATCAGATTGTGATGAGAAAATTTAAATTTTATTTCCAAATATAAT	665
Dp	380	ACAATATTTAAATTAATTAATTAATCTTTAATAATATAATATATATTTTAAATACAAAT	321
Qy	666	GA-TAATCAAAAGTGTGAACATTGTGAAAAGAGAGAAAAATTTAAATGATGAAAAATTTGTA	724
Dp	320	AATAATTAATATTAATTAATTAATGATTAATCTATTTAAATTAATTTTAAAGAAAAATTAAT	261
Qy	725	AACATCAATTTGTGAAATACAAATTTTGAAGTTGACAGAGAAAAAAACTGAAATTTCT	788
Dp	260	ATCTAATATATATTTTAAATACATAATTTTAAATTTGAAACATGACATAAATAGTATTCATAT	201
Qy	785	TATACATTTTCGGTACCAATTTTGGATCATTAAGAAATTAATCTGAAATCCATTCACAAAC	844
Dp	200	TAAATATATTTTATTAATATTAATTTAATAATTTAATA-----TGATGAATTAAG	153
Qy	845	TATTAATAATTAACAAAAATGATTAACCAACAAAAAAGAGAACATGACGATATTTGCTAA	904
Dp	152	TAAATTTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	93
Qy	905	AGAACATCATCATGATTAATAAAGACATGGCATATTAAGATTAAGAAACAAAACTA	964
Dp	92	TGATTAATATATATGTTTAATTAATTTTAAATCTTAATTAATTAATTAATTAATTAATTA	33
Qy	965	TTCAAAATCACAAAAATGATTA	986
Dp	32	TCTTTAATAATTAATTAATTAATA	11
RESULT	10		
	US-09-056-075-1		
	Sequence 1, Application US/09056075		
	Patent No. 5955368		
	GENERAL INFORMATION:		
	APPLICANT: Johnson, Eric A.		
	APPLICANT: Rodshaw, Marile		
	APPLICANT: Rood, Julian		
	TITLE OF INVENTION: Expression system for Clostridium		
	TITLE OF INVENTION: Species		
	NUMBER OF SEQUENCES: 2		
	CORRESPONDENCE ADDRESS:		
	ADDRESSEE: Quarles & Brady		
	STREET: 1 South Pluckney Street		
	CITY: Madison		
	STATE: WI		
	COUNTRY: US		
	ZIP: 53701-2113		
	COMPUTER READABLE FORM:		
	MEDIUM TYPE: Floppy disk		
	COMPUTER: IBM PC compatible		
	OPERATING SYSTEM: PC-DOS/MS-DOS		
	SOFTWARE: PatentIn Release #1.0, Version #1.30		
	CURRENT APPLICATION DATA:		
	APPLICATION NUMBER: US/09/056,075		
	FILING DATE:		
	CLASSIFICATION:		
	ATTORNEY/AGENT INFORMATION:		
	NAME: Seay, Nicholas J.		
	REGISTRATION NUMBER: 27386		
	REFERENCE/DOCKET NUMBER: 960296, 95238		
	TELECOMMUNICATION INFORMATION:		
	TELEPHONE: 608-251-9166		
	TELEFAX: 608-251-9166		
	INFORMATION FOR SEQ ID NO: 1:		
	SEQUENCE CHARACTERISTICS:		
	LENGTH: 6243 base pairs		
	TYPE: nucleic acid		
	STRANDEDNESS: double		
	TOPOLOGY: linear		
	MOLECULE TYPE: DNA (genomic)		
	FEATURE:		
	NAME/KEY: misc_feature		
	LOCATION: 3770..4013		

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;      OTHER INFORMATION: /note= "RP4 origin of DNA transfer (orit) from
;      OTHER INFORMATION: plasmid RP4"
US-09-056-075-1

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Query Match	3.3%;	Score 68.6;	DB 2;	Length 6243;
Best Local Similarity	47.0%;	Pred. No. 0.00029;		
Matches 256;	Conservative	0;	Mismatches 279;	Indels 10;
				Gaps 1.

QY	452	TGAACCTCAAGGTGTAATAATTGAAAGAAGAGAAAAATAAAAATGACATTTCATCGG	511.11
Db			
QY	392	ACATTAATCTCGGAATCAATATGTGATGAGAAAAATTTAAATTTCTCTTACACTTAAT	451.11
Db			
Db	860	ACTTTTAATTAATAAATGAAGATTTAAACTCTCATTTTATATTAAATTAAAAATGACGT	919.11
QY	452	TGAACCTCAAGGTGTAATAATTGAAAGAAGAGAAAAATAAAAATGACATTTCATCGG	511.11
Db			
Db	920	TTTATCAAAAAAATTTCCAAATATCCACACTAAGCCCAACAGCGCCCTATTAATATCCC	979.11
QY	512	AAATCAATTTGTGATGAGAAACCTTAAATTTTATTTAAATATATTAATGGAATTTCAAGT	571.11
Db			
Db	980	GCTTAAATCCCACTTTGAGACACTGTATATTTTACTTTAGCCCTAGTATATGATATATT	1033.11
QY	572	GTTAAATTTTGAAGAAGAGAAAAATTTAAATGACATTTTCATTCAAAATCAGATTGTGT	631.11
Db			
Db	1040	TTTATCAATTCATGCGACAGAAAAAATTAAGAAGGGGCACTATTAATAAAGTTCCCTGGAA	1099.11

QY	632	ATGAAAATTTTAAATTTTATTTCOA-----ATATATTGAAACCAAGGTGCA	681
Db	1100	CTACTTAAGTAAAAAATATCTTTACACACTCCCCAAAAAAGAACAGGTACAAAGTA	115
QY	662	ACATTTAGCAAAAGCAGAAAAATTTAAATGATGAAAAATTTGTAAACATCAATTTGTGAAA	741
Db	1160	CCCTTAATTAACAGCGTAAAAAATGAGCGTAAAAAATAAAAAATTTAAAAA	121
QY	742	TCAGATTTAGAGTTAGACAGCAAGCAAAAAAACAATGAAATTTGCTTATCTTTTCGTACA	801
Db	1220	TAAAAAATTAAAAAAATTAAAAAATTAAAAAATTAAAAAATTAAAAAATTA	127
QY	802	ATTTTGGCATCTAAAGAAATTTACTGAAATCCATATCAAAAACATATTATTAATTTACAAA	861
Db	1280	AAAAATTAAAAAATTAAAAAAATATTAATAATTAAAAAAATATTAATAATTAATAA	133
QY	862	ATGATTAATTAACCAAAAAAGAAAGAACATGACAGATATTTCTGTAAAGAACATCATATCTGATT	921
Db	1340	ATTAATAAATAATTAATAAATTAATAAATTAATAAATTAATAAATTAATAAATAATAT	139
QY	922	ATTA	926
Db	1400	AAAA	1404

RESULT 11
US-08-446-855A-1
; Sequence 1, Application US/08446855A

GENERAL INFORMATION:
APPLICANT: Stewart, Thomas S
APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
NUMBER OF INVENTION: phosphate synthetase II
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 1100 No. 5849573th Grebe Road, 8th Floor
CITY: Arlington
STATE: Virginia

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;
;      COMPUTER READABLE FORM:
;      DATE: 22-03-91
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.24

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1: CURRENT APPLICATION DATA:
2: APPLICATION NUMBER: US/08/446,855A
3: FILING DATE: 06-Jul-1995
4: CLASSIFICATION: 435
5: ATTORNEY/AGENT INFORMATION:
6: NAME: Milchard, Leonard C
7: REGISTRATION NUMBER: 29,009
8: REFERENCE/DOCKET NUMBER: 47-80
9: TELECOMMUNICATION INFORMATION:
10: TELEPHONE: 703-816-4000
11: TELEFAX: 703-816-4100
12: INFORMATION FOR SEQ. ID NO.: 1:
13: SEQUENCE CHARACTERISTICS:
14: LENGTH: 8920 base pairs
15: TYPE: nucleic acid
16: STRANDEDNESS: single
17: TOPOLOGY: linear
18: MOLECULE TYPE: genomic
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Query Match	3.3%;	Score 68.4;	DB 2;	Length 8920;
Best Local Similarity	44.8%;	Pred. No. 0.00032;		
Matches 304; Conservative	0;	Mismatches 371;	Indels 3;	Gaps 1;

OY	323	AAACCAAAACAATFCAACCTTTTGGCAACACTTTTCCAAAAATCCATTTTCGAAA	382
Db	114	AACGACGAAAGAGCTAAATTTTAAAGCATTTGACGAAAAATTAATTAATAAAAAA	173
OY	383	AAAAAATTTACATTACTTGGGAATCAAAATGTGTATGAAAAATTTAAATTCCTTC	442
Db	174	TAAAAAGATAAAAATATTTTATTTGATATGTATATATATATATATATATATTA	233
OY	443	ACCTATATTGAACCTCAAGCTTAAATTTAGAAAAAGGAAAAATTAACATGACA	502
Db	234	TACATTAATTAACAACTTTTTTTTTTTTTTTTTTCTTATATTTATTAACATCAT	293
OY	503	TTTCATCGGAATCAAAATTTGTATGAAAAACTTAAATTTTATTTAAATATATGA	562
Db	294	TAAATTTATTTATG	353
OY	563	ATTCAAAGTGT---TAAATTTACAAAAAGGAAAAATTTAAAGACCATTTCAATCA	619
Db	354	TGTTTATTTTATTTAAAAATTTACTGGAATATPAAACTTTATTAATATTTCCATTA	413
OY	620	ATCAGATGTGTATGAAAAATTTAAATTTTATTTTCAATATTAATGMAACTCAAGTGT	679
Db	414	ATGAATACAAATTATTAATTTTGTATGTACATTAATTAATTTTACACTCTATA	473
OY	680	GAACATTTAGAAAAAGCAAAAATTTAAATGATGAAAATTTGTAAACATCATTTCTGA	739
Db	474	ATMAAACCATCTTAATATTTTATACACAATATATATCTCCCAATATTTGTGTTCTAT	533
OY	740	AATCGAATTTAGAACTAGACAGAGAAAAAAACGAAATGTCTTATACTTTCCGTTA	799
Db	534	AATTTTATTTATATTTTATTTATTTAATTTTCATATTTTATTTTCTTAGTTTA	593
OY	800	CAATTTTGGGATCATAAAGAAATTTACTGAAATCCATATCAAAAATCTATTAATTTCAA	855
Db	594	TAAATATAGTAATCTTACTAAATTTAAAAAAGAAAAAAGAAAAAAGAAAAA	653
OY	860	AAATGATTAACCCAAAAAAGAAAGAACATCAGCATTTTGTGTAAGACATCATCTGA	919
Db	654	AAAAATTTTCATATGAAAAATGCACTGTATATGTAAATTTATATATTTTAAACATA	713
OY	920	TTTATAAAGAACATGCGCATATTAGATTTGAGAAACAAAAATCTATTCAAAATCACAAA	979
Db	714	ATATTAAGTATTAATAAAAAAAGAAAAAAGGAAAAAATAATATGATATATATATA	773
OY	980	ATGATTAACACATACAA 997	
Db	774	ATATATATATATATATA 791	

RESULT 12
US-09-150-741-1
; Sequence 1, Application US/09150741
; Patent No. 6183996
; GENERAL INFORMATION:
; APPLICANT: Stewart et al.
; TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
; Patent No. 6183996
; TITLE OF INVENTION: Synthetase II
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/150,741
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PL6380
; EARLIER FILING DATE: 1992-12-16
; EARLIER APPLICATION NUMBER: AU93/00617
; EARLIER FILING DATE: 1993-12-02
; EARLIER APPLICATION NUMBER: 08/446,855
; EARLIER FILING DATE: 1995-07-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8920
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-150-741-1

Query Match 3.3%; Score 68.4; DB 4; Length 8920;
Best Local Similarity 44.0%; Pred. No. 0.00032;
Matches 304; Conservative 0; Mismatches 371; Indels 3; Gaps 1;

QY 323 AAAACAAACAAATATCAAACTTTTTCGCAACAACTTTTTCGCAAAATTCATTCGAA 382
DB 114 aacgagagaaaggttaaaccttaagccttggaagaaataataaataa 173
QY 383 AAAAAATTCATTACTTCGCAATCAATTTGTATGAAATTTAAATTTCTTC 442
DB 174 taaagagataaaataatattgatatgagataatattgataatattgata 233
QY 443 ACCTATATGTAAGTCAAACTTTTAAATTTGAAAGAGAGAAATTAATTAATCA 502
DB 234 taacataagataaaacttttttttttttttttttttttttttttttttt 293
QY 503 TTTTCATGCGAATCAATTTGTATGAAATTTTAAATTTTAAATTTTAAATTTG 562
DB 294 taagtaattatataataataataataataataataataataataataata 353
QY 563 ATTCAAAGTGT--TAAATTTGAAAGAGAGAAATTTAAATTTGACATTTTCATTC 619
DB 354 tgcattctgtttataataatcttgaataataataataataataataataata 413
QY 620 ATCAGATTGTGTAAGAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAA 679
DB 414 atgaatacaattatataatattgagtgacacataatagtttaacctttata 473
QY 680 GAACATTTGAAAGAGAGAAATTTAAATTTGTAAGAAATTTGTAAGAAATTTG 739
DB 474 ataaaccatccatataatataacacataataataaccccaatattggttcc 533
QY 740 AATCAGAAATTTGAAATTTGACAGAGAGAGAAATTTGAAATTTGCTTAAATTT 799
DB 534 aattttatataatatttttttttttttttttttttttttttttttttttt 593
QY 800 CAATTTGGGATCAATTAAGAAATTTACTGAATTCATATCAAAACATTTATTAAT 859
DB 594 taaatagtaattcttaatttaaaaaaataaaaaaataaaaaaataaaaaa 653
QY 860 AATGATATTAACCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 919
DB 654 aaaaaattacataagaaataagactgtatatagttaatttaataattttaaca 713
QY 920 TTATAAAG 979

DB 714 atataatgtataaaaaaaatggaataataatagataataataa 773
QY 980 ATGATACACATACAA 997
DB 774 atataataataataa 791

RESULT 13
US-07-991-867B-41/c
; Sequence 41, Application US/07991867B
; Patent No. 5476781
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Hall, Richard L.
; APPLICANT: Gruidl, Michael E.
; TITLE OF INVENTION: No. 5476781e1 Entomopoxvirus Expression System
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESS: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/991,867B
; FILING DATE: 12-DEC-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92/14818
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,685
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/657,584
; FILING DATE: 19-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UFI14.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-991-867B-41

Query Match 3.2%; Score 66; DB 1; Length 1689;
Best Local Similarity 43.8%; Pred. No. 0.00072;
Matches 387; Conservative 0; Mismatches 490; Indels 7; Gaps 2;
QY 139 TGTATTAATTAATTAATTAATTTGATTCATTTTATATATGAAAGAGATATGA 198
DB 943 TATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 884
QY 199 TGAATTTGATTCATTTATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 258
DB 883 CGTACTCCAGTAACTAATTAATTAATTTCTGAATTTAATTAATTAATTAATTA 824
QY 259 AATTCATTAATTAATTTTTCGCAAACTTTTTCGAAATTTTCAATTTTCGAAATTA 318

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Page 11

QY 619 AATCAGATTGGCTATGAAAAATTAATTTTATTTATTTCAAAATATATGAAACTCAAAAGTG 678
 Db 463 ATTTTCCGAGTTTACAAAAAATATTAATTTCTCGAATCTTTTAATTAAGAGTTTAAAAA 404
 QY 679 TGAACATTTAGAAAAAGGAGAAAAATTAATAATGATGAAATTTGTGAACAAACATCATTTGTG 738
 Db 403 TGATATATATAAAAAATTAATAACTATTTACCAATACCGATATATAATATATATATATT 344
 QY 739 AATTCGAAATTTAGACGTAGACACAGAAAAAAACTGAAATGTCTATACTTTGGT 798
 Db 343 ATATCAATATTT---CGTGAATATATATAGAAACTGTAAATAATTTTAATTCGAGAC 288
 QY 799 ACAATTTGGCATCATTAAGAAATATGAGAAATCCATATCAATCAAAAACATATATATAATTACA 858
 Db 287 GAAAGATTTAATTTTGAACCTTTAGTTAATTTTGAAGAAATATCAAGTTTAAATGTT 228
 QY 859 AAAAAATGAATAAAACCAAAAAAAGAGAACAATGACGATATTTCTGTAAAGACATCATACTG 918
 Db 227 ATTTTAAT---GTTTAATATTTCTTATATATGAAATTTCTACCAAAACTTTAAAAACTA 171
 QY 919 ATTATTAAGAAACATTCGGCATATTTAGATTTGAGAAACAAAAAACTATTCAAAATTCACAA 978
 Db 170 GAGATTAATGAATTTAAAGCAATATATATATATATGAAAATATATATGTTAAAAAAAGTAAAG 111
 QY 979 AATGATTAACACATCAACAAGACATCAAGACATCAAGATCTTATTCACA 1022
 Db 110 TTTCGATATTTTCTTACCGCTGGATCTGAAGCAATATCATTCATTCAAA 67

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RESULT 15
5231168-1
: Patent No. 5231168
: APPLICANT: DZIEGIEL, MORTEN,BORRE, MARTIN;JEPSEN, SOREN.
: VUDST, JENS;RIENECK, KLAS;WIND, ANNETTE;JAKOBSEN, PALLE H.
: TITLE OF INVENTION: MALARIA ANTIGEN
: NUMBER OF SEQUENCES: 19
: * CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/409,658
: FILING DATE: 18-SEP-1989
: SEQ ID NO:1:
: LENGTH: 3095
5231168-1

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Query Match	3.2%	Score 66;	DB 6;	Length 3095;
Best Local Similarity	46.8%;	Pred. No. 0.00076;		
Matches 332;	Conservative	0;	Mismatches 355;	Indels 23; Gaps 3

[illegible]

Db	2505	tattattatataagaaaaataaaaataataattcttcttctttagttgttataataatc	2564
QY	524	GTATGAAAAACTTAAATTTTATTATTTAAATATATATGAAATTCAAAGTCTTAAATTTAG	583
Db	2505	taaaaataataataataataatagaacaattacagiatattattataatcgtgaagat	2624
QY	584	AAAAGAGAAAAATTTAAATGAACCATTTTCATTCCAAATGAGATTGGTATGAAAAATTTA	643
Db	2625	acatgataataaa--aaatttctgcgttataataataaataagaataattatcttta	2682
QY	644	AATTTTATTTCAATATATAATGAAACCTCAAGGTGAACTTTGAAAAAGAGCAAAAT	703
Db	2683	tgatattatttaagaatatataataatgataataaalgaaagaaagaaaaaaaat	2742
QY	704	TAAATGATGAAAATTTGTAAACATCAATTTGTCAATCAGAAATTTTGAAAGTTAGACAA	763
Db	2743	tttttatcatcttttccataaataatataaataattatataataataactgat	2802
QY	764	GGAAGAAAAAAGTCAATTTGTTTACTTTTTCGGTTACATTTTGGGATCA	813
Db	2803	aaatattatgatatataattataataataacatgltgccttcttggcataa	2852

Search completed: February 23, 2002, 08:37:21
Job time: 11899 sec

Page 11

Sat Feb 23 11:04:38 2002

us-09-636-826-1.rni

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2002, 05:14:42 ; Search time 1188.47 seconds

(without alignments)
18897.134 Million cell updates/sec

Title: US-09-636-826-1

Perfect score: 2090
Sequence: 1 GATATCACACATTCGTCAT.....TCGGCTTCTGCGTCTGCT 2090

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: em_estfun:*
2: em_esthum:*
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5: em_estpl:*
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9: em_hic:*
10: qb_est1:*
11: qb_est2:*
12: qb_hic:*
13: qb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	142	6.8	1885	10	BE420745
2	139.6	6.7	1036	13	CNS031MJ
3	139.4	6.7	879	13	CNS031JRG
4	136.8	6.5	1135	13	CNS031JRG
5	131	6.3	1139	13	AO897537
6	129.6	6.2	1101	13	CNS000SX
7	129.6	6.2	1201	13	CNS0167M
8	129	6.2	819	11	BS369277
9	129	6.2	1036	13	CNS00599
10	128.6	6.1	982	13	AO32557V
11	128.2	6.1	1101	13	CNS00EVL
12	128	6.1	990	13	CNS00601

C 13	127.8	6.1	1059	13	CNS0092B	AL097133 Drosophila
C 14	127.8	6.1	1337	5	BF630719	BF630719 HVSME001
C 15	126.2	6.0	834	13	B12387	B12387 F21E20-Sp6
C 16	125.4	6.0	757	10	AL514421	AL514421 AL514421
C 17	125.2	6.0	656	13	CNS012JA	AL174457 Tetraodon
C 18	125	6.0	614	13	CNS0152H	AL104165 Drosophila
C 19	125	6.0	1134	11	BF64906	BF64906 HV-CEA001
C 20	124.6	6.0	870	13	AO330286	AO330286 nbxb00465
C 21	124.2	5.9	1434	11	BS309133	BS309133 HVSME000
C 22	124	5.9	1101	13	CNS012JN	AL101645 Drosophila
C 23	122.6	5.9	945	13	CNS04DOK	AL285149 Tetraodon
C 24	122.4	5.8	1198	13	B08337	B08337 T19F9-Sp6.1
C 25	122.2	5.8	1101	13	CNS0153V	AL104965 Drosophila
C 26	121.8	5.8	859	13	A527955	A527955 ENTCM56TR
C 27	120.8	5.8	1223	13	B12981	B12981 T24D11-Sp6
C 28	120.6	5.8	850	13	A2186328	A2186328 SP-1006_B
C 29	119.4	5.7	888	13	CNS027EX	AL184578 Tetraodon
C 30	119.2	5.7	619	10	AL514935	AL514935 AL514935
C 31	119.2	5.7	907	13	CNS021J4	AL176953 Tetraodon
C 32	119	5.7	1079	13	CNS0351X	AL228786 Tetraodon
C 33	118.6	5.7	1042	13	CNS0148K	AL103838 Drosophila
C 34	118.4	5.7	974	13	CNS001TW	AL075432 Drosophila
C 35	117.4	5.6	1380	11	BS653591	BS653591 602582321
C 36	117.2	5.6	1185	11	BF273407	BF273407 GA_EB001
C 37	117	5.6	622	13	CNS04ROH	AL304226 Tetraodon
C 38	117	5.6	937	13	CNS0066L	AL062959 Drosophila
C 39	116.8	5.6	781	13	CNS009ND	AL053444 Drosophila
C 40	116.8	5.6	864	13	CNS00ANBY	AL298519 Tetraodon
C 41	116.8	5.6	930	11	BS67946	BS67946 HVSME1001
C 42	116.4	5.6	901	11	BF64987	BF64987 HV-CEA001
C 43	116	5.6	576	13	CNS0256N	AL181688 Tetraodon
C 44	115.4	5.5	782	13	CNS06RMZ	AL412161 T7 end of
C 45	115.4	5.5	875	13	A2184435	A2184435 SP-1003_A

ALIGNMENTS

RESULT 1
LOCUS BE420745 1885 bp mRNA EST 24-JUL-2000
DEFINITION HMM002.B02 ITEC HMM Barley Leaf Library Hordeum vulgare cDNA clone
ACCESSION BE420745
VERSION BE420745.1 GI:9418588
KEYWORDS EST
SOURCE EST
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
1 (bases 1 to 1885)

REFERENCE

Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier
S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,
Herrmann, R.G., Holton, T., Jacquemont, J.M., Jia, J., Jondreville, P.,
Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y.,
Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,
Sorrells, M., Warburton, M., and Wenzel, G.
International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)

JOURNAL

COMMENT Botantesches Institut der LMU
Menzinger Str. 67, D-80638 München GERMANY
Fax: 49 30 171683
Email: hermann@botanik.biologie.uni-muenchen.de
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
1. 1885

FEATURES

source
/organism="Hordeum vulgare"
/culturvar="Barke"
/db_xref="taxon:4513"

D	b	249	AAA	308
Oy		370	CCATTTCAGAAAATAATTTACATTAACTCGGAATCAAAATTGTGTAAGAAAATTT	429
D	b	309	AAA	368
Oy		430	AAATATTCCTTCACTATAATTGAACCTCAAGTGTTAAATTTAGAAGACAGAAAAA	489
D	b	369	AAA	428
Oy		490	TAAAAATGACCATTTCATGCGAAATCAAATGTGTATGAAAAACTTAAATTTTTTTT	549
D	b	429	AAA	488
Oy		550	AAATTAATTAATTCAAATTCGAAAGTGTTAAATTTGAAGAAAGCAAAAATTTAAATGCACAT	609
D	b	489	AAA	548
Oy		610	TTCAATTCAAAATTCAGATTGTGTATGAAAAATTTAAATTTTATTCAAATATTAATTGAAA	669
D	b	549	AAA	608
Oy		670	CTCAAGTGTGACATTAGAAAAAGCAGAAAAATTTAAATGATGAAAATTTGTAAACAT	729
D	b	609	AAA	668
Oy		730	CAATTTGTGAATTCAGATTTAGAGTTAGACAGCAAAAGAACTGATGTCTTTATAC	789
D	b	669	AAA	728
Oy		790	TTTTGGTTCACAATTTGGCATATAGAAATTTACTGAATCCATATCAAAAACCTATT	849
D	b	729	AAA	788
Oy		850	TAAATTCGAAAATGAAATTAACCAAAAAAGAGAACATGACGATTTTGTGTAAGAC	909
D	b	789	AAA	848
Oy		910	ATCATCTGATTATTAAGAACATCGCATTTAGATTTGAGAAACAAGAACTATTCAA	969
D	b	849	AAA	908
Oy		970	AATCACAAAATGATATACACACTACAAAGACATGAAAAGATCTTATTCCAATAATGA	1029
D	b	909	AAA	968
Oy		1030	GGTGAACTTAATTAAGTAA 1047	
D	b	969	AAAAAAAAAAAAAAAAAAAAA 986	

RESULT 3
 CNS01JRG/c 879 bp DNA GSS 12-JUN-2001
 LOCUS Anopheles gambiae GSS AT end of clone 14D07 of NotreDame1 Library
 DEFINITION from strain PST of Anopheles gambiae (African malaria mosquito),
 genomic survey sequence.
 ALI47405
 ACCESSION ALI47405.1 GI:7005551
 VERSION
 KEYWORDS African malaria mosquito,
 Anopheles gambiae
 ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
 Culicoidae; Anophelinae;
 1 (bases 1 to 879)
 REFERENCE Genoscope.
 TITLE Direct Submission
 AUTHORS Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage ;
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 REFERENCE 2 (bases 1 to 879)
 AUTHORS Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.

TITLE	Journal	COMMENT	FEATURES
Submitted (16-FEB-2000) B.M.T., Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France		This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.	
source	1.879	/organism="Anopheles gambiae" /strain="PEST" /db_xref="taxon:7165" /clone="14D07" /clone_lib="Notredame1" /note="end : 77"	Location/Qualifiers
BASE COUNT	66 a	38 c	1 g 670 t 104 others
ORIGIN			
Query Match	6.7%;	Score 139.4;	DB 13; Length 879;
Best Local Similarity	43.9%;	Pred. No. 4.5e-08;	
Matches 360;	Conservative 47;	Mismatches 404;	Indels 9; Gaps 1
283	AAACCTTTGCAAAATATCCATGTCGGAATATAATTTGAAAAACAACAATATCAAC	342	
Db	AAATTTTAAAAAAATTTATATAAAAAAATATAAAAAAAGTAGTAA	814	
343	CTTTTGCACACCTTTACAAAAATCCATTTTCAGAAAAAAATTTACATTAACTTG	402	
Db	TATATTGGAAATGWTAAATAAAAAAGAAAAAAGAAAAAAGTAAATATAAAAA	754	
403	CGAAATCAATTTGTATGAAAAATTTAAATTTCTTTCACCTAATTAATGCAACGCA	462	
Db	RAATATGTAAGAAKMAAAATATAGTAAAAAARATGAGMAMDKKMKMAAAAGCTRA	694	
463	GGTTTAAATTTAGAAAGAGAAAAATAAAAATGACCATTTCATGCGAAATCAATTG	522	
Db	KKGMAAAAAAATAAAAAAGKATATAAAAAAGAAAAAAGAAAAAAGAAAAA	634	
523	T-----GTATGAAAACTTAAATTTTATTAATATTAATGAATTCAAAGTGT	573	
Db	TTATATKMKMKMAAGAAAAATTTGMMGKTDAAAAAATTTGAAAAAAGAGAA	574	
574	TAAATTTAGAAAGAGAAAAATTTAAATGACATTTCATTCAAAATCAGATTGTAT	633	
Db	GKAGAGKRGARAAAGAGCAKAKAAAAAATAATGTTAARAATGAAAAAARAKKAT	514	
634	GAAATTTAAATTTTATTTCAATATATATGAAACGAAAGTGGAACATTGGA	693	
Db	RAAAAAAAMKAGDAAKRGWAGAAAAARAGATMKAKAAAAAATAATTTDAAAA	454	
694	GGAGAAAAATTAATATGATGAATTTGTAAACATCAATTTGGAATCAGAAATTTGA	753	
Db	TTAMWTBAAAAAAGAKAKATKTGDBRAAAAAAADAANANAAAAA	394	
754	AGTTGACAGAGAAAAAACTGAAATTTGCTTATACCTTTGCGTTACAAATTTGGATCA	813	
Db	AAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAA	334	
814	TAAAGAAATTTACTGAATTCATATCAAAAACTATTATTAATTAACAAAAATGAATTAAC	873	
Db	AAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAA	274	
874	AAAAAAGAGACATGACGATTTTCGTAAGAACAATCATCTGATTATTAAGACAT	933	
Db	AAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAA	214	
934	GGCATTTATTAATTTGAGAAACAAAACTTTCAAAATCCAAAAATGATTAACAAT	993	
Db	AAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAA	154	
994	ACAAAGAACATGAAGAATCTTATTCACAAAAATGAGAGCTGAACCTTAATCTAACTTGA	1053	

Db	153	AAATATAAAAAAAAAAAAAAAAAAATAAAAAAAAAAATATANAAAAAAAAAAAAAAAAANNNNNNNNN	94
OY	1054	TTTTCACTTTATTACTTACTTACTTATTAAGCCCTAAAAATA	1093
Db	93	NAAANNCAMBTMTTANNNAANNAANNNNTATNAAAAAAAAAAAA	54
RESULT	4		
CNS0336Q			
LOCUS			
DEFINITION	CNS0336Q	1135 bp DNA GSS	15-MAY-2000
	Tetradon nigroviridis genome survey sequence PUC-Ort end of clone		
	208P24 of library G from Tetradon nigroviridis, genomic survey		
	sequence.		
ACCESSION	AL226115		
VERSION	AL226115.1	GI:7885026	
KEYWORDS	GSS; genome survey sequence.		
SOURCE	Tetradon nigroviridis.		
ORGANISM	Tetradon nigroviridis		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;		
	Tetraodontidae; Tetradon.		
REFERENCE	1 (bases 1 to 1135)		
AUTHORS	Roeßl-Crollius,H., Jallion,O., Dasilva,C., Fizesac,C., Fisher,C., Bonneau,H., Billault,A., Quétier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis		
TITLE	Unpublished		
JOURNAL	2 (bases 1 to 1135)		
REFERENCE	Roeßl-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizesac,C., Wincker,P., Brodier,P., Quétier,F., Saurin,W. and Weissenbach,J. Human gene number estimate provided by genome wide analysis using Tetradon nigroviridis DNA sequence		
TITLE	Unpublished		
JOURNAL	3 (bases 1 to 1135)		
REFERENCE	Genoscope.		
AUTHORS	Direct Submission		
TITLE	Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases		
JOURNAL	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetradon .		
COMMENT	Location/Qualifiers		
FEATURES	Source		
	1..1135	/organism="Tetradon nigroviridis"	
	/db_xref="taxon:99883"		
	/clone="208P24"		
	/note="Genoscope sequence ID : C0AG208DH1SP1-end ; PUC-Ort"		
BASE COUNT	863 a 65 c 43 g 124 t	40 others	
ORIGIN			
Query Match	6.5%; Score 136.8; DB 13; Length 1135; Best Local Similarity 47.6%; Pred. No. 8e-08; Matches 351; Conservative 14; Mismatches 373; Indels 0; Gaps 0;		
OY	310	AAATAAATTGGAAAACAACAATATCAAACTTTTGCGACACACTTTTACAAAAT	369
Db	248	AA	307
OY	370	CGATTTTCGAGAAAAAAATTTACATTACTTCGCGAATCAAAATGTGATGAAAAATTT	429
Db	308	AA	367
OY	430	AAATTTTCCTTACCCTATTAATTGAAGCTCAAAGTGTAAATTTAGAAAAAGAGAAAAA	489
Db	368	AA	427
OY	490	TAAAAAATGACCATTCATGCGAAATCAAAATGTGTATGAAAAAACTTAAATTTATTTT	549

[illegible]

FEATURES

Location/Qualifiers
 source 1. 1139
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate-3153 Col-14 Row-A"
 /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 157 a 42 c 79 g 746 t 115 others
 ORIGIN

Query Match 6.3%; Score 131; DB 13; Length 1139;
 Best Local Similarity 48.9%; Pred. No. 3.9e-07;
 Matches 366; Conservative 0; Mismatches 378; Indels 5; Gaps 2;

QY 310 AATTAATTTTGAACAAACAAATATCAACCTTTTGGCAACACTTTTACAAAAT 369
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1058 AATTAATTTTGAACAAACAAATATCAACCTTTTGGCAACACTTTTACAAAAT 999
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 370 CCATTTTCAGAAAAAAATTTACATTAACCTTGGCAATCAATTTGTTGAAAAATTT 429
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 998 ATTAATTTATTAATAAAAAATTTTAAAAATTTAAAAATTTAAAAATTTAAAAA 939
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 430 AAAAAATTTCTTACCTATATTTGAACCTCAAGTGTAAATTTAGAAAGGAGAAAA 489
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 938 AAAAAATTTAAAAACATATTAATAAAAAATTTAA-----TAAAAAATTTAAAAA 883
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 490 TAAAAATGACCTTTCATGCGAATCAATTTGTTGTTGAAAACTTAAATTTTATTTT 549
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 882 AAAAAATTTAAAAATTTATTAATAAAAAATTTAAAAATTTAAAAATTTAAAAA 823
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 550 AATTAATTTGAATTTCAAGTGTAAATTTTGAAGAGAGAAAAATTTAAATGACAT 609
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 822 GAAAAATTTAAAAATTTATTAATAAAAAATTTAAAAATTTAAAAATTTAAAAA 763
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 610 TTCAATTAATAATGATTTGTATGAAAAATTTAA-ATTTTATTTCAATATATTTGA 668
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 762 TAAATTAATAAAAAATTTAAAAATTTATTAACAAATTTATTAATTAATAATA 703
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 669 AATCAAGTGTGAACATTTTGAAGAGAGAAAAATTTAAATGATGAAATTTTGAACA 728
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 702 AATTAATTTATTAATTTATTAATAAAAAATTTAAAAATTTAAAAATTTAAAAA 643
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 729 TCAATTTGTAATGCAATTTTGAAGTGTAGACAGAAAAATTTGAATTTCTTATA 788
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 642 ATAAATATTAATAAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAA 583
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 789 CTTTTCGTTACATTTTGGGATCAATTAAGAAATTTACTGAATTCATATCAAAATCTAT 848
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 582 AATTAATAAAAAATTTATTAATAAAAAATTTAAAAATTTAAAAATTTAAAAA 523
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 849 ATAAATTTACAAATGATTAACCAAAAAATTTAAACACATGCGATTTTCTTAAGAA 908
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 522 AAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAA 463
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 909 CATCATAGTATTTAAAGAACATCGCATTTTGAATTTGAAGAACAAATCTTTCA 968
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 462 AAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAA 403
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 969 AATTCACAAAAATGATTAACACATTAACAAGAACATGAAGAATCTTATTCACAAATG 1028
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 402 AAGGAAANNANNAAAAAATTTAAAAATTTTTTTTTTTTTTTTTTAAAAAAT 343
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 1029 AGTGAATTAATTAATTAATTTTATTTT 1057
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 342 TATTAATTTTATTTTATTTTATTTT 314
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
 CNS000SX/c CNS000SX 1101 bp DNA GSS 03-JUN-1999
 LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR02106 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

AL050813
 AL050813.1 GI:4930826

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 1101)

AUTHORS

Genoscope.

COMMENT

Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
 Determination of this BAC (end) and sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1. 1101
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_id="RPCI-98"
 /clone="BACR02106"
 /note="end : TET3"

BASE COUNT 77 a 26 c 85 g 768 t 145 others
 ORIGIN

Query Match 6.2%; Score 129.6; DB 13; Length 1101;
 Best Local Similarity 45.5%; Pred. No. 5.8e-07;
 Matches 318; Conservative 33; Mismatches 347; Indels 1; Gaps 1;

QY 310 AATTAATTTTGAACAAACAAATATCAACCTTTTGGCAACACTTTTACAAAAT 369
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 721 AAAAAACCTTAATAAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAA 662
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 370 CCATTTTCAGAAAAAAATTTTACATTAACCTTGGCAATCAATTTGTTGAAAAATTT 429
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 661 AATTAATAAAAAATTTATTAATAAAAAATTTAAAAATTTAAAAATTTAAAAA 602
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 430 AAAAAATTTCTTACCTATATTTGAACCTCAAGTGTAAATTTAGAAAGGAGAAAA 488
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 601 ATTAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 548
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 489 ATAAATTTGACCAATTTTCGCAATCAATTTGTTGTTGTTGTTGTTGTTGTTT 548
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 541 ACAATTAATAAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAA 482
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 549 TAAATTAATTTGAATTTAAAGTGTAAATTTTGAAGAGAGAAAAATTAATTAATTA 608
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 481 AAAAAATTTTAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAA 422
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 609 TTTCATTAATAATGATTTGTATGAAAAATTTAAATTTTATTTCAATATTTGA 668
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 421 AAAAAATTTTAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAA 362
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 669 ACTCAAGTGTGAACATTTTGAAGAGAGAAAAATTTAAATGATGAATTTTGAACA 728
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[illegible]

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FEATURES
  source      Seq primer: AATTACCCCTCAGTAAGG
              High quality sequence stop: 787.
              Location/Qualifiers
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                  /organism="Hordelum vulgare"
                  /cultivar="Morex"

```

/db_xref="taxon:4513"
 /clone="HVSME10023121f"
 /clone_lib="Hordem vulgare 20 DAP spike EST library
 HVCN0010 (20 DAP)"
 /issue_type="20 DAP spike"
 /lab_host="SOLR"
 /note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI; For
 more details on library preparation and sequence analysis
 see <http://www.genome.clemson.edu/projects/barley/10>
 order a clone see <http://www.genome.clemson.edu/orders>"

BASE COUNT 12 a 47 c 26 g 734 t

Query Match 6.2% Score 129; DB 11; Length 819;
 Best Local Similarity 48.4%; Pred. No. 8e-07;
 Matches 357; Conservative 0; Mismatches 380; Indels 0; Gaps 0;

QY 311 AATAAATTTTGAACAAACAAATATCAACCTTTTGCAGCACTTTTACAAATC 370
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 812 AAAAAAAAAACAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAG 753
 QY 371 CATTTTCGAGAAAAAATTTACATTACCTTGCAGAAATCAATTTGTATGAAAAATTTA 430
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 752 AAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 693
 QY 431 AATTCCTTCACTTAATTTGAACCAAGCTTAATTTGAAGAAAGAGAAAAAT 490
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 692 AAAAAAGTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 633
 QY 491 AAAAAATGACATTTTCATGCGAAATCAATTTGTATGAAAAAATTTTATTTTA 550
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 632 AGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 573
 QY 551 AATTAATTTGAATCAAGCTTAATTTGAAGAAAGAGAAAAATTTAATGACATT 610
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 572 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 513
 QY 611 TCATTCAAAAATGATGTATGAAAAATTTAATTTTATTTCAATTAATTTGAAC 670
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 512 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 453
 QY 671 TCAAGTGTGAATTTAGAAAAAGAGAAAAATTTAATGAGAAAAATTTGTAACATC 720
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 452 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 393
 QY 731 AATTTGGAATGAGATTTAGAGTTAGACAGAAAAAAGCTGAATTTGTTTACT 790
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 392 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 333
 QY 791 TTTCGTTCAATTTTGGGATCATAAAGAAATTAAGTAATTCATTAATCTTAT 850
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 Db 332 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 273
 QY 851 AATTTCAAAAAATGATTAACCAAAAAAGAGAAATGATGATTTTCTGTAAGAGACA 910
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 272 AGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 213
 QY 911 TCATTCAGTTAATTAAGAAATGCGCATTTGTAATTTGGAACAAAAAATCTATTCAA 970
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 212 AAAAAAAGAAAAAAGAAAAAAGAGAGGAGAAAAAAGAAAAAAGAAAA 153
 QY 971 ATCACAAAAAATGATTAACCAATCAAGAAATGAGAAATCTTATTCACAAATGAGAG 1030
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 152 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 93
 QY 1031 GTGACCTTAATCTAA 1047
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 92 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 76

RESULT 9
 CNS00599/c

LOCUS CNS00599 1036 bp DNA GSS 03-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR1116 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL057797
 VERSION AL057797.1 GI:4932579
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1036)
 REFERENCE
 AUTHORS Direct Submission
 TITLE Genoscope.
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail: secrefgenoscope.cns.fr)
 - Web: www.genoscope.cns.fr

COMMENT
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazuhiro Osoegawa and
 Aaron Mammeter in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
 pl and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
 source
 1..1036
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR1116"
 /note="end : TET3"

BASE COUNT 64 a 56 c 41 g 701 t 174 others

Query Match 6.2% Score 129; DB 13; Length 1036;
 Best Local Similarity 42.4%; Pred. No. 7e-07;
 Matches 334; Conservative 62; Mismatches 389; Indels 2; Gaps 1;

QY 257 AAAAAATTCATTAATTTTCCCAAACTTTTGCAGAAATATCATGTTGGAATTA 316
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 785 AAGCAACATTAATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 726
 QY 317 TTTGAAAAAACAATATCAACCTTTTGCAGAACTTTTACAAATCATTTT 376
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 725 AAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 666
 QY 377 CAGAAAAAATTTTCACTTAATTTGCAATTTGATGAAAAATTTAATTTT 436
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 665 MAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 606
 QY 437 CCTTCACCTAATTAATTTGAACTCAAGTGTAAATTTAGAAAGGAAAAATTA 496
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 605 AAAAAAATTCGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 548
 QY 497 TGACCATTTTCATGCAAAATTTGATGAAAAAATTTTATTTTAAATATA 556
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 547 STRAATTTTAAKAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 488
 QY 557 ATTGAATTCAGTAAATTTAGAAAGGAGAAAAATTTAATGACATTTTCATT 616
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 487 AKAKAATKBTBKBAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 428
 QY 617 AAAAAATGATGTATGAAAAAATTTTAAATTTTATTTCAATTAATTTGAACTCAAG 676

Db	427	TAAAGMGAATKKKRAARAGAAKAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	368
QY	677	TGTGAACATTTCAGAAAAAGAGAAAAAATTAAATGATGAAATTTGTAAACATCAITTTG	736
Db	367	AAA	308
QY	737	TGAAATCAGATTTCAGAGTTAGACAAGAAAAAAACGATTTGTCTTATCTTTGGC	796
Db	307	AAA	248
QY	797	TTCAATTTTGGGTCATTAAAGAAATTTACTGAAATCCATCAAAACATATTATTA	856
Db	247	AAA	188
QY	857	CAAAATTCGATTAAACCAAAAAAAAAAGAGAACATGACGATTTTGGTAAAGAACATCATAC	916
Db	187	AAA	128
QY	917	TGATTATAAAGAACATCGCCATATTAGATTGAGTTCAGACAAAAAACTATTCAAATTCACA	976
Db	127	AAADAAAAAAAAAAAAA	68
QY	977	AAAAATGCATACCAATACCAAGAACATGAAAGAACTTATTCACAAAAATGGAAGTGAAC	1036
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QY	1037	TTAAATA	1043
Db	7	WTWAAA	1

BASE COUNT	141 a	69 c	43 g	674 t	55 others
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Query Match	6.2%;	Score 128.6;	DB 13;	Length 982;
Best Local Similarity	45.8%;	Pred. No. 8.1e-07;		
Matches 377;	Conservative	0;	Mismatches 441;	Indels 5;
				Gaps 1;

[illegible]

QY 566 CAAGAGTGTAAATTTTGAGAAAGACAGAAATTAATGACCAATTGATCAAAATGACA 625
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 QY 626 TTGTGTATGAGAAATTTAAATTTTATTTTCAGAAATATATATGAAACTCAAGTGAACAT 685
 Db 737 AAAMAAWAAATWAAWATATATWATATATATWATWATWAAWAAWAAWATATATAT 796
 QY 686 TTGAGAAAGAGAGAAATTTAAATGATGAAATTTTGTAACATCAATTTGTGAATCAG 745
 Db 797 WAAMAAWAAATWAAWATATATWATATATATWATWATWAAWAAWAAWATATATAT 856
 QY 746 AATTTGAGAACTTGACAG 805
 Db 857 WTATATWATATWATATWATATWATATWATATWATATWATATWATATWATATWAT 916
 QY 806 TGGGATCATTAAGAAATTTAGTGAATTCATATCAAAAACATTTATATAATTCAGAAATGA 865
 Db 917 WAAAAAAG 976
 QY 866 ATAAACAG 925
 Db 977 ATATWATWATATWATATATWATWATATWATATATATATATATATATATATATAT 1036
 QY 926 AAGACATGCGCATTTAGCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 985
 Db 1037 TATWATWATWATATWATATWAAWAAATTAATWATATATATWATWAAWAAWAAWAAW 1096
 QY 986 AACAA 990
 Db 1097 AWWAA 1101
 RESULT 12
 CNS00601/C
 LOCUS
 DEFINITION
 DROSOPHILA melanogaster genome survey sequence Teth end of BAC #
 BAC14123 of RPCI-98 library from Drosophila melanogaster (fruit
 fly) genomic survey sequence.
 AL065624
 AL065624.1 GI:4944693
 GSS.
 fruit fly.
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 990)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
 Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazuhiro Osoegawa and
 Aaron Mammosier in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 Location/Qualifiers
 1..990
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 FEATURES
 source

D _b	270	AAA	211
Q _y	846	ATTTAATAATACAAAATAAGTAAATCCAAAAAAGAGACATGCGATTTCGTAA	905
D _b	-210	AAA	151
Q _y	906	GACCATCATCTGATTATTAAGAACATGGCGATTATTGAATTTGCAGAACAAAAACTAT	965
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Q _y	966	TCAAAATCACAAAATGGATTACACATACAAGAAACATGAAGAATCTTATTCCAAA	1025
D _b	90	AAVANAAGA	31
Q _y	1026	TGGAGTGCACTTAA	1040
D _b	30	WAAAGNAAAAAAAAA	16

ID	BF630719/c	standard; RNA; EST; 1337 BP.
AC	BF630719;	
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SV	BF630719.1	
XX		
DT	21-DEC-2000 (Rel. 66, Created)	
DT	21-DEC-2000 (Rel. 66, Last updated, Version 1)	
XX		
DE	HVSMED0013H16f Hordeum vulgare seedling shoot EST library HVCDNA0002 (Dehydration stress) Hordeum vulgare cDNA clone HVSMED0013H16f, mRNA sequence.	
XX		
EST		
XX		
OS	Hordeum vulgare (barley)	
OC	Euraryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.	
XX		
RN	[1]	
RP	1-1337	
RA	Wing R., Close T.J., Kleinhofs A., Wise R., Begum D., Frisch D., Yu Y., Anderson H., Dale J., Henry D., Kernodle S., Palmer M., Rambo T., Sasaki C., Schwartzbeck J., Simmons J., Choi D.W., Main D., Wood T.; "Development of a genetically and physically anchored EST resource for barley genomics"; Unpublished.	
XX		
CC	Contact: Wing RA	
CC	Clemson University Genomics Institute	
CC	Clemson University	
CC	100 Jordan Hall, Clemson, SC 29634, USA	
CC	Tel: 864 656 7288	
CC	Fax: 864 656 4293	
CC	Email: twing@clemson.edu	
CC	Seq primer: AATTAAACCTCCTACTAAGGC	
CC	High quality sequence start: 38	
CC	High quality sequence stop: 1204.	
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FH	key	Location/Qualifiers
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FT		/cultivar="Morex"
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FT		/lab_host="TUC121"

[illegible]

QY	74	ATTTCACATTAATCGACATTAATTAAGTGTGAAAAAGGACATTAATGGAATTAAGTTGAA	133
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QY	134	AAGGCTGTTTATATATTAATAGACTTAATTTGATTCATTTTCATATATCTGAAAAACAAGT	193
Db	1186	TAAACATTTTATATATTAATTAATTAATATCAACAACATATATTAATCTTTATTAATATAA	112
QY	194	ATGTATGAATTTGATTTATTTATGACCTGATGAAAAAGTTAAGATTTAGTCTTTT	253
Db	1126	TAAATACAAATANTAAAAATATACAAATATATTAATTAATAAATACAAATATATAGTAATAAAT	106
QY	254	TTTAAATTTCCAAATTTAAATTTTGGCCAAACCTTTTGCCAAATATCCATGTCGGAAAT	313
Db	1066	AAATAAATATATATCAAAATTTGAAATATAAAAAACAATATTAATATTAATAATATTAAT	100
QY	314	AAATTTGAAAAACAAAACAATATCAACCTTTTGGCAACATTTTTCAGAAAAATCCAT	373
Db	1006	TAAATATATTAATTAATAAATAAATAAATAAATAAATAATAGATTAATAATATATATAA	947
QY	374	TTTCGAAAAAATAATTTACATTA--ACTTGGCAATTCAAATTTGCTATGAAAAATTTA	430
Db	946	TATATATTAATATATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	887
QY	431	AAATTTCCCTTCCACTTAATTTGAAGCTCAACAGCTTAAATTTAGAAAAAGCAAAAT	490
Db	886	AAAAACAATGATA--AGATTTATACATTAATAATATATATATGATATATAATATAAT	829
QY	491	AAAAATGACCATTTTCATGCGAAATCAAAATTTGTATGAAAAACTTAATTTTATTTTA	550
Db	838	ATAATATATTAATTAATATATACACACACATCTAATTAATAAATAATTAATATATTA	769
QY	551	AATATTAATGAAATTCAAAGTGTAAATTTAGAAAAAGCAAAATTTAAATGACCAAT	610
Db	768	AATATTAATTAATTAATTAACAAATTTAAAAAATATTAATAAATAAATAATTAATTAAT	709
QY	611	TCATTCAAAAATCAGATTTGTATGAAAAATTTTAAA-----TTTTTATTTCCAAATATTAATG	666
Db	708	TAAATTAATAAATATTAATAAATAAATAAATAATTAATTAATTAATTAATTAATTAAT	649
QY	667	AAACTCAAAAGTGTACACATTTAGAAAAAGCAAAATTTAAATGATGAATTTGTAA	726
Db	648	AAAAATAAAAAATAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	589
QY	727	CATCAATTTGGAATCAGATTTAGAAAGTTAGACAAAGAAAAAATTAATTAATTAATTAAT	786
Db	588	ACAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATC	529
QY	787	TACTTTTCGGTTACAAATTTTGGTCATCAAGAATTTAGCAATTCATATCAAAAACTA	846
Db	528	AAATTAATGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	469
QY	847	TTTATTAATTAACAAATATGATTAATAAACCAAAAAAGAGACATGAGCATTTTCTGAAG	906
Db	468	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	414
QY	907	AACATTCATAGATTATTAAGAACAATGGCCATTTAGAAATTTGAGAAACAAAAAACTAT	966
Db	413	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	354
QY	967	CAAAATCAAAAAATGATTAACAACATACAAAGACATGAAGAATCTTATTCACAAAT	1026
Db	353	AAAAATAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	294
QY	1027	GGAGGTAACTTAATATCTACTTTCGATTTTCAGTTTATTAATTAATTAATTAATTAATTAAT	1086

Db 293 CAAAAAAAAAAAAAAAACTTTTAAATAATTTTAAATAATAA 234
 QY 1087 AAAAAA 1093
 Db 233 AAAAAA 227

RESULT 15

B12387/c

LOCUS B12387 834 bp DNA GSS 14-MAY-1997
 DEFINITION F21E20-Sp6.1 IGF Arabidopsis thaliana genomic clone F21E20, DNA
 sequence.

ACCESSION

B12387

B12387

B12387.1

GI:2093671

GSS.

thale cress.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 834)
Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and
 Ecker, J.

BAC End Sequences at ATGC

Unpublished (1997)

Other_GSSs: F21E20-Sp6, F21E20-Sp6.2

Contact: Ecker J.

Arabidopsis Thaliana Genome Center

University of Pennsylvania
 Dept. of Biology, University of Pennsylvania, Philadelphia, PA
 19104
 Tel: 215-898-9384
 Fax: 215-898-8780
 Email: jecker@atgenome.bio.upenn.edu

Seq primer: Sp6

Class: BAC ends

High quality sequence start: 409

High quality sequence stop: 422.

Location/Qualifiers

1. 834

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/strain="Columbia"

/db_xref="taxon:3702"

/clone="F21E20"

/sex="hermaphrodite"

/note="Vector: BelobACII; Site_1: EcoRI; Site_2: EcoRI;
 Produced by Thomas Altmann"

BASE COUNT 35 a 37 c 25 g 583 t 154 others

ORIGIN

Query Match 6.0%; Score 126.2; DB 13; Length 834;
 Best Local Similarity 41.2%; Pred. No. 1.7e-06;
 Matches 284; Conservative 0; Mismatches 406; Indels 0; Gaps 0;

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 QY 438 CTTTCACTTAATTTGAACCTCAAGTGTAAATTTAGAAAAAGAGAAAAAT 497
 Db 771 AA 712
 QY 498 GACCATTTTCATGCAATCAATTTGTGTGAAAAAATTTTAAATTTAA 557
 Db 711 AA 652
 QY 558 TTGAATTTCAAGTGTAAATTTAGAAAAAGAGAAAAATTTAAATGACCATTTCA 617
 Db 651 AA 592

QY 618 AATTCAGTCTGTATGAAAAATTTTAAATTTTCAATATATTTGAACGCAAGT 677
 Db 591 AA 532
 QY 678 GTGAACATTTAGAAAGAGAAAAATTTAAATGTGAATTTGTAAACATCAATTTGT 737
 Db 531 AA 472
 QY 738 GAATCAGATTTAGAGCTTGACAGAGAAAAAACTGAATTTCTTATCTTTTGGT 797
 Db 471 NAANNANNN 412
 QY 798 TACATTTTGGGATCATTAAGAAATTTACTGAATTCATCAAAACATTTATTAATTAC 857
 Db 411 AA 352
 QY 858 AAAAAATGAATTAACCAAAAAAGAGAACATGACATATTGCTAAAGACATCAATCT 917
 Db 351 AA 292
 QY 918 GATTATTAAGACATGCGCATTTAGATTTGAGAACAAAAAACTTTCAAAATCACAA 977
 Db 291 NAANNANNN 232
 QY 978 AATGATTAACACATACAAAGAACATGAAGAATCTTATTCACAAAAATGAGGCTGACT 1037
 Db 231 AA 172
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